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Result
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1,
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6: /cgn2_6/ptodata/1,
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PCT-US-33-08528-45
US-08-858-876A-4
US-09-472-880-4
US-09-077-675A-13
US-09-077-675A-13
US-09-077-675A-5
US-09-077-675A-5
US-09-077-675A-5
US-09-077-675A-5
US-09-077-675A-3
US-09-261-599B-3
US-09-456-455A-3
US-09-461-599B-3
US-09-463A-1
US-08-488-876A-2
US-09-413-426-2
US-09-413-426-2
US-09-413-426-2
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RESULT 2 US-08-118-270-45 ; Sequence 45, Application US/08118270

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PCT-US93-08528-45
; Sequence 45, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248633
INFORMATION FOR SEQ ID NO:
                  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                    TITLE OF INVENTION:
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APPLICATION NUMBER: US,
FILING DATE: 09-SEP-19:
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APPLICATION NUMBER: US 0
FILING DATE: 10-SEP-1992
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TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Murphy, Randall B. APPLICANT: Schuster, David I.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TELEPHONE: 202-737-3528
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                                                                                                                                                                                                                                  FMSFLFPMLVISILNTVIANKLTV 199
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                                                                   New York University
WENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
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BROWDY AND NEIMARK
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                                                    RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%; Score 304; DB 1; Length 353; 33.3%; Pred. No. 1.9e-20; Indels
                                    348
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RESULT 4
US-08-858-876A-4
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Daniel (
APPLICANT: Pascale
APPLICANT: Pascual
APPLICANT: Vita NA
                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                            Sequence 4, Application US/08858876A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                   TITLE OF INVENTION: Type 2 Neurotensin Receptor TITLE OF INVENTION: (hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                    219 FLFYLLPMTVISVLYYLMALRVSI 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 248633
                              CITY: Washington STATE: D.C.
               COUNTRY:
                                                            STREET:
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202 - TELEPHONE: 202-737-3528
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 VSVVYVPIFVVGVIGNVLVCLVILQH---QAMKTPTNYYLFSLAVSDLLVLLLGMPLEVY 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Townsend, Kevin
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                       FMSFLFPMLVISILNTVIANKLTV 199
                                                                                                                                                                                                                                                                                                                                                                               RTKKFISAIWLASALLAIPMLFTLGLQNR--SGDGTHPGGLVCTPIVDTATVKVVIQVNT 175
                                                                                                                                                                                                                                                                                                                                                                                                              RALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTS 218
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                                                           400 Seventh Street
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Pascual FERRARA
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                                                                                                                                                   Vita NATALIO
                                                                                                                                                                                                 Daniel CAPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                         Jacobson, Price,
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Pred. No. 1.9e-20;
Pred. No. 1.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MURPHY-2 PCT
                                                                         Holman
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                                                                         Stern,
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                                                                         PLLC
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COMPUTER READABLE FORM:

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09472880 Patent No. 6274333 GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 WSHYPWVFGDLGCRGYYF---VRELCAYATVLSVASLSAERCLAVCQPLRARRLLTPRRT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 TALYSLIFAFGTAGNALSVHVVLKARAGRPGRLRYHVLSLALSALLLLLLVSMPMELYNFV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1997
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                                                                 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 (hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Type 2 Neurotensin Receptor
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               APPLICATION NUMBER: US/09/472,880 FILING DATE: 28-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                            ADDRESSEE: Jacobson, Price STREET: 400 Seventh Street
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Pascual FERRARA
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Pred. No. 3e-18;
                                                                                                                                                                                                                                                                                Price, Holman & Stern,
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Best Local Simple 72;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,049 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               ZIP: 07065-0900
COMPUTER READABLE FORM:
                                                  ATTORNEY/AGENT INFORMATION:
NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 WRNYPFLFGPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRA 160
                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 3-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                    REFERENCE/DOCKET NUMBER:
                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln Ave
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: proteir
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LENGTH: 416 amino acids
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NAME: Player, William E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09077675A
                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee-Yuh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrew D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%;
                                                  42,452
                                                                                                                                                                                                   US/09/077,675A
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                                    19590P
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Pred. No. 3e-18;
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RESULT 7
US-09-077-675A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09077675A
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                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pai, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                 REFERENCE/DOCKET NUMBER: 19. TELECOMMUNICATION INFORMATION: T32-594-1273
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 732-594-4720
                                                                                                                             NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 3-JUN-1998
                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 VTATCVALEVVGIAGNILITMLVVSRERELRTTTNLYLSSMAFSDLLIFLC-MPLDLVRLW 104
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P.O. Box 2000, 126 E. Lincoln Ave
361 amino acids
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Pred. No. 4.6e-18;
47; Mismatches 69;
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US-09-077-675A-13; Sequence 13, Application US/09077675A; Patent No. 6242199
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APPLICANT: Pai, Lec
APPLICANT: Feighner
APPLICANT: Howard,
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                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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CITY: R
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            STRANDEDNESS:
TOPOLOGY:
                                          LENGTH:
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                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                              amino acid
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                                           366 amino acids
                                                                                                         732-594-4720
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Van Der Ploeg, Leonardus
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linear
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           single
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Pred. No. 5.9e-18;
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US-09-077-675A-13

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Best Local Similarity
 Best Local Similarity
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                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 353 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: COCUZZO, Anna L.
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                            TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.U.
                                                                                                                                                                                                                                            NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wil
                                                                                            STRANDEDNESS:
                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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P.O. Box 2000, 126 E. Lincoln Ave.
                                                                                                                            353 amino acids
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Pong, Sheng-Shung
Van Der Ploeg, Leonardus H.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Howard, Andrew D.
                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                              linear
                                                              protein
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                                                                                              single
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31.7%; Pred. No. 6e-18;
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21.7%;
31.7%;
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                                                                                                                                                                                                                                            19590₽
Score 274; DB 4; Pred. No. 1.1e-17;
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                                                Matches
                                                              Query Match
Best Local S
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                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein -077-675x-10
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 LVIWAVAFCSAGPIFVLVGVE---HDNGTDPRDTNECRATEFAVRSGLLTVM---WWV--- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 RNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRIL 164
TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                           NAME: COCUZZO, Anna L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                   TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIVWGFSVLFSLPNTSIHGIKFHYFPNGS------LVPGSATCTVIKPMWIYNF 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
                                                                Similarity
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                                                                                                                                                                                   364 amino acids
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Howard, Andrew D.
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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                                                              21.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/077,675A
                                                                                                                                                                                                                                                                                                             42,452
                                            47;
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                                              Score 274; DB 4;
Pred. No. 1.1e-17;
7; Mismatches 69
                                                                                                                                                                                                                                                                                                .9590P
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                                                                             Length 364;
                                              Indels
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; TOPOLOGY: lin
; MOLECULE TYPE:
US-09-077-675A-5
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US-09-077-675A-5
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
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ADD...
STREET: ...
STREET: Rahway
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                                                                      45 VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
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                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                                                                                                                                               ENGTH:
                                                   VTATCVALFVVGIAGNLLTMLVVSRFREMRTTTNLYLSSMAFSELLIFLC-MPLELFRLW 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIQVTSFLFYLLPMTVISVLYYLMALRV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTATCVALEVVGISGNLLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLC-MPLDLVRLW 103
                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                             289 amino acids
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                                                                                                                           Conservative
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                                                                                                                                                                                                                             linear
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                                                                                                                                     21.6%; Score 273; DB 4; 31.7%; Pred. No. 1.1e-17;
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                                                                                                                     Mismatches
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                                                                                                                                                       Length 289;
                                                                                                                     Indels
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                                                                                                                    Gaps
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US-07-629-1041-3
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Best Local :
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                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (203)268-195
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 3.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gershengorn, Marvin C
APPLICANT: Straub, Richard E
TITLE OF INVENTION: PITUITARY TRE
NUMBER OF SEQUENCES: 3
                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                 229
                                                                                  175
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                                                                                                                                                                                                                                                                                                                     Local Similarity hes 72; Conserv
                                                                                                                    97
                                                                                                                                                                              42 GNIMYVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDSIYGSW-----VYGYV
                                                                                                                                                                                                 59 GNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 IIQVTSFLFYLLPMTVISVLYYLMALRV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 QYRPWNLGNLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
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AMPRET: 25 Skytop Drive
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ISVLYYLMA 237
                                                                           SLPNTSIHGIKFHYFPNGSLVPGSATC----TVIKPMWIYNFIIQVTSFLFYLLPMTV 228
                                                                                                                                GCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLF 174
                                                                                                                                                                                                                                                   MENDTVSEMNQTELQPQAAVALEYQVVTILLVVIICG-----
                                             CMLWFFLLDLNISTYKNAVVV----SCGYKISRNYYSPIYLMDFGV-----FYVVPMIL
                                                                                                              GCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIY 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-456-455A-3
                                                                                            SEQ ID NO 3
LENGTH: 259
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/22
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.1
LEQ ID NO 3
LEQ ID NO 3
LENGTH: 259
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application Patent No. 6395877
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                   APPLICANT: Glucksmann, Maria A.
APPLICANT: Tsai, Fong Ying
TITLE OF INVENTION: 14273 Receptor, A No. 6448005el G-Protein Coupled Receptor
FILE REFERENCE: MNI-204CP3
CURRENT APPLICATION NUMBER: US/09/456,455A
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14273 Receptor, A No. 6395877el G-Protein Coupled Receptor
FILE REFERENCE: 5800-4B, 035800/177086
CURRENT APPLICATION NUMBER: US/09/261,599B
CURRENT FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/107,761
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/223,538 PRIOR FILING DATE: 1998-12-30
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15
OTHER INFORMATION: Description of Unknown Organism: Seven OTHER INFORMATION: Transmembrane Segment Rhodopsin Superfamily
                                                                      ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: OTHER INFORMATION:
                                                 FEATURE:
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Transmembrane Segment Rhodopsin
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Pred. No. 8.7e-17
8; Mismatches 6
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Superfamily
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; MOLECULE TYPE: US-08-288-663A-1
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Best Local Similarity
Matches 67; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                      APPLICATION NUMBER: 286986/
APPLICATION NUMBER: 286986/
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215
TITING DATE: 22-DEC-1993
                                                                                                                                                                                                                                                                                                 NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/288,663A FILING DATE: 09-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION TITLE OF INVENTION: AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STREET: 13
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                               TOPOLOGY:
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HOSOYA, Masaki
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                                                                 amino acids
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TITLE OF INVENTION: No. 6436703el Nucleic F.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790C1P2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
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PRIOR APPLICATION NUMBER: 09/540,217
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   -, Lee-Yuh
---APPLICANT: Feighner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shan-
APPLICANT: Van P-
TITIE --
                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/077,675A FILING DATE: 3-JUN-1998 CLASSIFICATION:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                            APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                       COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                      STREET: P.O. CITY: Rahway
                                                                                                                                                                                                   ZIP: 07065-0900
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                     ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGACCACCGCGCTCCTTCTTCTGCCTGCCCATGGCCATCATGAGCGTGCTCTACCTG
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RESULT 4
US-09-077-675A-9
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                                                                     Sequence 9, Application US/09077675A
Patent No. 6242199
GENERAL INFORMATION:
APPLICANT: Pai, Lee-Yuh
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LENGTH: 1088 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                       APPLICANT:
                                                       APPLICANT:
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        APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 732-594-4720
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Feighner, Scott C.
Howard, Andrew D.
Pong, Sheng-Shung
Van Der Ploeg, Leonardus H.T.
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Pred. No. 4.2e-18;
0; Mismatches 261;
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Best Local S
Matches 290
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                       492
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STRANDEDNESS:
TOPOLOGY: lin
     804
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STREET: P.O. Box 2000, 126
CITY: Rahway
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
mes 290; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 732-594-4720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COCUZZO, Anna L. REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1122 base pairs
                                                                                                                                                         CATCCTACACCCGTTCCGCGCCCAAACTGCAGAGCACCCGGCGCCCGGGCCCTCAGGATCCT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGCACGAGAACGGCACCGACCCTTGGGACACCAACGAGTGCCGCCCCCACCGAGTTTGC
                                   CAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACCTGTACGGTCAT
                                                                                                                                                                                                                                                                              GCAGTACCGGCCCTGGAACTTCGGCGACCTCCTCTGCAAACTCTTCCAATTCGTCAGTGA
                                                                                                                                                                                                                                                                                                                                                                  GGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCCTGGAGGTCTATGAGATGTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGTGGTGTCGCGCTTCCGCGAGCTGCGCACCACCACCAACCTCTACCTGTCCAGCAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCGTCATCTGGGCCGTGGCCTTCTGCAGCGCCCGGGCCCATCTTCGTGCTAGTCGGGGT
                                                                                                      CGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCAT 551
                                                                                                                                                                                                          GAGCTGCACCTACGCCACGGTGCTCACCATCACAGCGCTGAGCGTCGAGCGCTACTTCGC
                                                                                                                                                                                                                                            GACCGTGTGCTTCGCCTCCATCCTCAGCATCACCGTCAGCGTGGAGCGCTACGTGGC 431
                                                                                                                                                                                                                                                                                                              GCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGA 371
                                                                                                                                                                                                                                                                                                                                              GGCCTTCTCCGAT----CTGCTCATCTTCCTCTGCATGCCCCTGGACCTCGTTCGCCTCTG
                                                                                                                                        CATCTGCTTCCCACTCCGGGCCAAGGTGGTGGTCACCAAGGGGCGGGTGAAGCTGGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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linear
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52.3%;
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126 E. Lincoln
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 302; Conserv
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                                                                                                                                                                                                                                             LENGTH: 1063 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             NAME: COCUZZO, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                           157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Led
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                       252 GGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTG 311
                                                                                                                                        132 CGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAATGTCCTGGTGTG 191
                                                                                        192
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                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln Ave.
                                                     GCTGGTAGTGTCACGCTTCCGCGAGATGCGCACCACCACCAACCTCTACCTGTCCAGCAT 216
                                                                               CCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCT 251
                                                                                                              CGTCACCGCCACCTGCGTGGCGCTCTTCGTGGTGGGTATCGCGGGCAACCTGCTCACGAT 156
GGCCTTCTCCGACCTAC---TCATCTTCCTCTGCATGCCCCTCGACCTCTTCCGGCCTCTG
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Feighner,
                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/077,675A
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                                                                                                                                                                      Score 114; DB 4; L
Pred. No. 1.1e-16;
O: Mismatches 270;
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273
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                                                  TELEX:
                                                                   TELEFAX:
          LENGTH:
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GENERAL INFORMATION:
APPLICANT: Pai, Lec
APPLICANT: Feighner
APPLICANT: Howard,
APPLICANT: Pong, SI
APPLICANT: Van Der
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                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         FILING DATE: 3-JUN-1
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Cocuzzo, Anna L.
                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
                                                                                                                               TELEPHONE: 732-594-1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 GGAGCATGATAACGGCACTGACCCTCGGGACACCAACGAGTGCCGCGCGCACGGAGTTCGC
                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 GCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGA
                                                                                                                                                                                            NAME: COCUZZO, Anna L. REGISTRATION NUMBER: 42,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. CITY: Rahway
                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000, 126 E. Lincoln Ave.
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nucleic acid
                      1029 base pairs
                                                                                                          732-594-4720
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Howard, Andrew D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                     3-JUN-1998
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STRANDEDNESS: Sil;
TOPOLOGY: linear
HOLECULE TYPE: CDNI
US-09-077-675A-4
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US-08-086-439C-2
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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chio, Christopher L.
APPLICANT: Huff, Rita M.
TITLE OF INVENTION: A Synthetic Gene
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 301;
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 52.1 nes 301; Conservative
                                                                                                                                                                               CITY: Kalamazoo
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                        ADDRESSEE: The Upjohn Company, ADDRESSEE: Property Law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGCTTCCCGCTGCGGGCCAAGGTAGTGGTCACCAAGGGCCGGGTAAAGCTGGTCAT
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                                                                                                                                                           Michigan
                                                                                                                                                                                                      301 Henrietta
                                                                                                                                      USA
      PatentIn Release #1.0,
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Pred. No. 2.4e-16;
0; Mismatches 271;
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      Version #1.25
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                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                    Sequence 2, Application US/08434877 Patent No. 5721132 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-85-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 616-385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO:
                                                                                                      TITLE OF INVENTION: A Synthetic Gene TITLE OF INVENTION: Receptors NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                             APPLICANT: Chio, Christopher APPLICANT: Huff, Rita M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
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ADDRESSEE: The orj-
ADDRESSEE: Property Law
ADDRESSEE: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 616-385-6897
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                                                             The Upjohn Company,
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139 GTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTG
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Intellectual
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RESULT 9
US-08-475-742-3
; Sequence 3, Application US/08475742
; Patent No. 6121015
; GENERAL INFORMATION:
; APPLICANT: O'Malley, Karen L
; APPLICANT: Todd, Richard D
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Best Local Similarity
Matches 236; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1 July 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: 3-434-877-2
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REGISTRATION NUMBER: 33.673
REFERENCE/DOCKET NUMBER: 47.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616.385-5210
                                                                                                                                                                   532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 TACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTG 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Gateway 2000, P5-90
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1161 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette (DS, HD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Michigan
                                                                                                                                                                 GGCCGCGACCCCGCCGTGTGCC
                                                                                                                                                                                   CACTACTTCCCCAATGGGTCCC
                                                                                                                                                                                                                                ACGTGGCTGCTGTCCGCGGCGGCGCGCGCGCCCGTACTGTGCGGCCTCAACGACGTGCGC
                                                                                                                                                                                                                                                                                                      GTGCCGCTGCGCTACAACCGGCAGGGTGGGAGCCGCCGGCAGCTGCTCATCGGCGCC 471
                                                                                                                                                                                                                                                                                                                          CACCCGTTCCGCGCCAAACTGCAGAGCACCCGGGGGCGCCGCGGGCCCTCAGGATCCTCGGCATC 498
                                                                                                                                                                                                                                                                  GTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTC 558
                                                                                                                                                                                                                                                                                                                                                                           TGCACCGCCTCCATCTTCAACCTGTGCGCCCATCAGCGTGGACAGGTTCGTGGCCGTGGCC 411
                                                                                                                                                                                                                                                                                                                                                                                                TGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGCTACGTGGGCGATCCTA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGCGTGGCTGAGCCCCCGCCTGTGCGACGCCCTCATGGCCATGGACGTCATGCTG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCTGGCGGTC 258
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53.4%;
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Pred. No. 2.5e-16;
0; Mismatches 206;
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RESULT 10
US-08-056-051-1
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Best Local Similarity 53.4%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 08/014,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Gene Encoding the Rat Dopamine FILE REFERENCE: WU 102 CON DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Van tol, H. H.
AUTHORS: Bunzow, J. R.
TITLE: Cloning of the gene for a human dopamine D4 receptor
TITLE: with high affinity for the antipsychotic clozapine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)..(1367)
OTHER INFORMATION: D4 Dopamine Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGES: 610-614
DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: Nature VOLUME: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
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                                                                         638 GGCCGCGACCCCGCCGTGTGCC 659
                                                                                                                                                                                                                                                                                                                                                                                       398 GGCGCGTGGCTGAGCCCCCGCCTGTGCGACGCCCTCATGGCCATGGACGTCATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 GTGGTGTATGTGCCAATTTTTTGTGGTGGGGGGTCATTGGCAATGTCCCTGGTGTGCCTGGTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 TCTGACCTCCTGGTCCTGCTTCGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCCGCTGCGCTACAACCGGCAGGCTGGGAGCTGCGCCGCAGCTGCTGCTCATCGGCGCC
                                                                                                              CACTACTTCCCCAATGGGTCCC 580
                                                                                                                                                                              GTCTGGGGCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTC
                                                                                                                                                                                                                                                      CACCCGTTCCGCCCAAACTGCAGAGCACCCCGGCGCCCTCAGGATCCTCGGCATC
                                                                                                                                                                                                                                                                                                           TGCACCGCCTCCATCTTCAACCTGTGCGCCATCAGCGTGGACAGGTTCGTGGCCGTGGCC
                                                                                                                                                   ACGTGGCTGCCGCGGCGGCGGCGCGCCCGTACTGTGCGGCCTCAACGACGTGCGC
                                                                                                                                                                                                                                                                                                                                TGCTTGGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTA 438
                                                                                                                                                                                                                                                                                                                                                                                                                              TACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGACCTCCTCGCTCTCCTGGTGCTGCCGCTCTTCGTCTACTCCGAGGTCCAGGGT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGCCACCGAGCGCGCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCCTGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCTGGCGGTC 258
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Pred. No. 2.5e-16;
0; Mismatches 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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Sequence 1, Application US/08056051 Patent No. 5516683 GENERAL INFORMATION:

APPLICANT:

Grandy,

David

APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/056,
FILING DATE: 1930429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1370 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Van Tol, Hubert H.-M.
TITLE OF INVENTION: A No. 5516683el Human Dopamine Receptor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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518 GTGCCGCTGCGCTACAACCGGCAGGGTGGGAGCCGCCGGCAGCTGCTCATCGGCGCC
                                                                                                                                                                                                                                                                                                                                                                       139 GTGGTGTATGTGCCAATTTTGTGGTGGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID STRANDEDNESS: sing TOPOLOGY: linear
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                    CACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCCGGGCCCTCAGGATCCTCGGCATC 498
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                                                                 TACCCTTTCTTGTTCGGGCCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTG 378
                                                                                                                                                                                                          GCCGACCTCCTCCTCCTCCTGCTGCTGCCGCTCTTCGTCTACTCCGAGGTCCAGGGT 397
                                                                                                                                                                                                                                             TCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAAC 318
                                                                                                                                                                                                                                                                              GTGGCCACCGAGCGCCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCCTGGCGGCC
                                                                                                                                                                                                                                                                                                                                                     TGCTTCGCCTCCATCCTCAGCATCACCGTCAGCGTGGAGCGCTACGTGGCCCATCCTA 438
                                                                                                                                        GGCGCGTGGCTGAGCCCCCGCCTGTGCGACGCCCTCATGGCCATGGACGTCATGCTG
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Pred. No. 2.5e-16;
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US-07-928-611-17
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TELEX: 810-221-8317
TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1-ENGTH: 1370 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Appli
Patent No. 5569601
                                                                                                                                      Query Match
Best Local Similarity
Matches 236; Conserv
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APPLICANT: Van Tol, Hubert |
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000 TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: NO. 5569601nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                             FEATURE:
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NAME/KEY:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                 199 ATTCTGCAGCACCAGGCTATGAAGACGCCCACCACTACTTACCTCTTCAGCCTGGCGGTC 258
                                                                                      139 GTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTTGCCTGGTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10 Sou
CITY: Chicago
STATE: Illinoi
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278 GTGGCCACCGAGCGCCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCCTGGCGGCC
                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 199201 CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
                                                                                                                                                                                                                                                                               LOCATION:
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                                                                    60606
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10 South Wacker Drive, Suite 3000
                                                                                                                                        Conservative
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                                                                                                                                    Score 112.4; DB 1;
Pred. No. 2.5e-16;
0; Mismatches 206;
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                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1370 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Civelli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A NO. 5883226el Human Dopamine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                FEATURE:
                                                                                                                     FEATURE:
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MEDIUM TYPE: Floppy
                                                                   FEATURE:
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 53(
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NAME/KEY:
                              LOCATION:
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                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                   LOCATION:
                                                                                                     NAME/KEY:
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                  NAME: NO. 5883226nan, Kevin REGISTRATION NUMBER: 35,303
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                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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RESULT 13
US-09-060-694-17
; Sequence 17, Application US/09060694
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Best Local Similarity
Matches 236; Conserv
            TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6203998nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 6203998el Human Dopamine Receptor and Uses
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Civelli, APPLICANT: Van Tol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518
                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 GGCCGCGACCCCGCCGTGTGCC
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                                                                                                                          APPLICATION NUMBER: US/09/060,694
FILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
TELEFAX:
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CITY: Chicago
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                 STATE:
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312-913-0002
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Pred. No. 2.5e-16;
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; FEATURE:
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US-09-060-694-17
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US-09-378-074-17
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Patent No. 6437114
GENERAL INFORMATION:
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LENGTH: 1370 base pairs
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LOCATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                              TITLE OF INVENTION: A NO. 6437114el Human Dopamine Receptor NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                 APPLICANT: Van Tol, Hubert H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCAAGTTC
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                                     COUNTRY: USA
ZIP: 60606
                                                                        STATE: Illinois
                                                                                       CITY: Chicago
                                                                                                          ADDRESSEE: Allegretti & Witcoff, Ltd. STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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1268..1370
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53.4%;
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Pred. No. 2.5e-16;
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Best Local Similarity
Matches 236; Conserv
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TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                    638
                                                  559 CACTACTTCCCCAATGGGTCCC 580
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APPLICATION NUMBER: 07/928,611
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                  GGCCGCGACCCCGCCGTGTGCC
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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53.4%; Pred. No. 2.5e-16;
tive 0; Mismatches 206
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Search completed: January 17, 2003, 02:35:14 Job time: 61 secs
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PCT-US93-07370-17
Sequence 17, Applicat.
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT:

APPLICANT:

TITLE OF INVENTION: A Novel Human Dopamine Receptor and Uses NUMBER OF SEQUENCES: 22

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
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NAME/KEY:
                                                                    638 GGCCGCGACCCCGCCGTGTGCC
                                                                                                  559 CACTACTTCCCCAATGGGTCCC 580
                                                                                                                                   578 ACGIGGCIGCIGCCGCCGCGCGCGCGCCCCTACIGTGCGGCCTCAACGACGIGCGC 637
                                                                                                                                                           499 GTCTGGGGCTTCTCCGTGCTCTCCCCGGCCAACACCAGCATCCATGGCATCAAGTTC 558
                                                                                                                                                                                                                   518
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104..1267
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Maximum Match 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1				_						Result
125	9 125	3 125	7 125	5 125	5 125	125	3 1252	2 125	1 126	. Score
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415	415	415	415	412	412	296	293	249	242	Query Match Length DB
22	21	21	21	22	22	22	22	22	22	DB
AAG63353	AAY52992	AAB02830	AAY71296	AAB67805	AAB67803	AAB67806	AAB67807	AAG80937	AAB68333	ID
Amino acid sequenc	Human neurotensin-	Human G protein co	Human orphan G pro	Amino acid sequenc	Amino acid sequenc	Splice variant of	Splice variant of	Human nGPCR15. Ho	Amino acid sequenc	Description

of	6265	22	412	26.4	w	45
o acid sequen	Υ5	21	412	26.4	333	44
G pro	285	21	412	σ.	w	43
form	AAB62653	22	386	26.4	w	42
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la G-	898	22	660	6	ω	40
la melano	168	22	660	6	w	39
la	898	22	595	7.	5	38
la melano	169	22	595	7.	ū	37
	896	22	428	ω	1	36
osophila melan	ABB64752	22	428	ω ·	$\vdash$	35
D. melanogaster pe	696	22	419	ω.	$\vdash$	ω 4
e FM-3.	918	22	405	7.	9	33
<u>,</u>	64	21	405	7.	9	32
te	63	22	439	0.	4	31
Rat FM-3. Rattus	19	22	412		4	30
Rat G-protein coup	53	22	413	1.	4	29
Human G-protein co	ω	23	426	ω.		28
	56	22	445	ω.	.7	27
_	52	22	445	ω.	.7	26
te	52	22	426	53.9	.0	25
FM-3.	9918	22	403	Ü		24
growth ho	464	21	403	ω.		23
Human mutant G pro	67	21	403	Ψ		22
۵	53	21	403	Ψ		21
Z Z	26	23	395	1	033.	20
	w	22	395	1.	ω.	19
acid sequen	36	22	395	1.	033.	18
Human NMUR2 protei	6	23	415	9	25	17
G-pro	AAU77155	23	$\mathbf{L}$	9.	25	16
	AAB67804	22	415	9.	25	15
acid sequen	0	22	415	9.	25	14
- G-pr	0362	22	415	9.	25	13
GTP-binding	6429	22	415	99.1	1252	12
Amino acid sequenc	AAG63366	22	415	99.1	25	11

## ALIGNMENTS

AAB68333 RESULT 1 G-protein coupled receptor; obesity; signal transduction; diabetes; metabolic disease; neurological disease; psychotherapy; dermatology; urogenital disease; inflammation; cancer; tissue repair; photoageing; skin pigmentation; frailty; osteoporosis; cardiovascular disease; gastrointestinal disease; infection; allergy; respiratory disease; sensory organ disorder; sleep disorder; hair loss; gene therapy; (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC 08-OCT-1999; 11-APR-2001 EP1090990-A1. PFI-002 Amino acid sequence of human g-protein coupled receptor PFI-002. 09-JUL-2001 ААВ68333; AAB68333 standard; Protein; Harland L; 06-OCT-2000; Homo sapiens. (first entry) 2000EP-0308852 99GB-0023888 242 AA

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RESULT 2
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Best Local !
                                                                                                                                                                                                                  G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder;
WO200136473-A2
                                                                                                                                          cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder, Alzheimer's disease; cance attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human G-protein coupled receptor. The G-protein coupled receptor polynucleotide and polypeptide are useful as pharmaceuticals or in the manufacture of medicaments for the treatment of obesity. They are useful in the diagnosis and treatment of diseases and disorders associated with signal transduction such as obesity diabetes and metabolic disease, neurological disease, psychotherapeutics, urogenital disease, inflammation, cancer, tissue repair, dermatology, skin pigmentation, photoageing, frailty, performance of the statement of the protein and th
                                                  Homo
                                                                                                                                                                                                                                                                                                                                                          Human nGPCR15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG80937 standard; Protein; 249
                                                                                                  neuroprotective
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                                                                                                                       rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human G-protein coupled receptor (GPCR) polynucleotides and polypeptides, for screening modulators of the polypeptide useful in treating diseases associated with signal transduction, e.g. cancer, inflammation, or especially, obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-302046/32
N-PSDB; AAF85107.
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42; Conservative
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                                                                                                                          disorder;
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08 - MAY 2000
                                                                                                                                                       disorder affecting the brain or a genetic predisposition, specifically schizophrenia. ngPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of ngPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and
                                                                       treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease migraine and senile dementia. Additional disorders include inflammatory
                                                                                                                                                                                                                                                     The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a discourage of the coding sequences are useful for screening a human to diagnose a
Sequence
                           conditions (e.g. Crohn's disease), rheumatoid arthritis, disorders, cancers, respiratory ailments such as asthma, diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogeli G,
Schellin
                                                                                                                                                                                                                                                                                                                                                                          Claim 37; Page
                                                                                                                                                                                                                                                                                                                                                                                                         New G protein-coupled polynucleotide useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-389826/41.
N-PSDB; AAH50977.
                                                                                                                                          hormonal disorders. Modulators of nGPCRx activity have the utility for
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17-NOV-1999;
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99US-0173396
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99US-0166071
                                                                                                                                                                                                                                                                                                                                                                          261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ПРЈОНИ СО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parodi LA,
PS, Bannig
                                                                                                                                                                                                                                                                                                                                                                                                    receptor (nGPCR-\mathbf{x}) and its encoding for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bannigan CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hiebsch
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Sejlitz T, Huf
                                          and inflammatory
                                                             autoimmune
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                                                                                                                                      Best Loc
Matches
                                                                                                                                                             Query Match
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                      121
                                              63
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                                                                                     MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
         ALFETYCFASILSITTYSVERYYAILHPERAKLQSTRRRALRILGIVWGFSVLFSLPNTS
ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                            VLVCLVILQHQAMKTPNTYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                          VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                      l Similarity
240; Conser
                                                                                                                                      Conservative
                                                                                                                                              99.1%;
                                                                                                                                      0,.
                                                                                                                                             Score 1252; DB 22;
Pred. No. 2.3e-141;
                                                                                                                                      Mismatches
                                                                                                                                                         Length
                                                                                                                                    Indels
                                                                                                                                                          249;
                                                                                                                                    0;
                                                                                                                                    Gaps
                    180
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182
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RESULT 3
AAB67807
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
           polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular disease (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, lumune disorders, allergies, sepsis or gynecological disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; str. cardiovascular disease; heart failure; angina pectoris; obesity; emes; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; seps:
                                                                                                                                                                                                           The present sequence represents a splice variant of the short version a human G-protein coupled receptor designated IGS4A. IGS4 exists in topolymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB67807 standard; Protein; 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gynecological
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                                                                                                                                                                                                                                                                          Example 1b;
                                                                                                                                                                                                                                                                                                                                                  New G-protein coupled receptors and the
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF80327
                                                                                                                                                                                                                                                                                                                                                                                                                              Deleersnijder W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001
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                                                                                                                                                                                                                                                                                                                                       useful
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                                                                                                                                                                                                                                                                                                                                       for
   cardiovascular system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                      cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                  preventing, ameliorating
                                                                                                                                                                                                                                                                        Page 96-97; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99NL-1013140
2000EP-0202683
2000US-0222047
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   skeletal
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                                                                                                                                                                                                                                                                                                                                                                                                                      c,
                                                                                                                                                                                                                                                                                                                   the polynucleotides encoding or correcting nervous system dyslipidemias, inflammations,
   muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                            Nys
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 thyroid,
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gastrointestinal lung or
                                                                                                                                     diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 emesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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RESULT 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                              24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                                                            WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                          New G-protein coupled receptors and useful for preventing, ameliorating disorders, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genitourinary system, or immunological disease. are useful as diagnostic reagents for detecting overexpression or altered expression of IGS4.
                                  or cancers
                                                                                                                                                                                                                                                                                                                                        gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                               Splice variant of G-protein coupled receptor IGS4A long version.
                                                                                                                                                                                                                                          25-SEP-2000; 2000WO-EP09584.
                                                                                                                                                                                                                                                                   12-APR-2001
                                                                                                                                                                                                                                                                                          WO200125269-A2
                                                                                                                                                                                                                                                                                                                  Homo
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                                                                                                                                                      (SOLV ) SOLVAY PHARM
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                                                                                            2001-273568/28.
DB; AAB80326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALFETYCFASILSITTYSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                              2000EP-0202683
2000US-0222047
                                                                                                                               ξ
                                                                                                                                                                                                                                                                                                                                         disorder
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                                                                                                                                                                                                                  99EP-0203140
                                                                                                                                                                                                      99NL-1013140
                                                                                                                               Berger
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99.6%;
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Pred.
                                                                                                                              Loeken
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No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No
.
                                          the polynucleotides encoding or correcting nervous system dyslipidemias, inflammations,
                                                                                                                               Ç
                                                                                                                              Nys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
.8e-141;
                                                                                                                               G
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                                                                                                                              Venema
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                                            pain
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Example

1b;

Page

92-93;

English

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RESULT 5
AAB67803
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               24-SEP-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular disease; heart failure; angina pectoris; obesity; emesimotility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of G-protein coupled receptor IGS4A short version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypertension), dyslipidemias, obesity, "emesis, gastrointestinal disorders (e.g. inflammations bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, overexpression or altered expression of IGS4.
                                                                                                                                                                                                                                                                      12-APR-2001
                                                                                                                                                                                                                                                                                                                                                          WO200125269-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a splice variant of the long version of a human G-protein coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilopsy, bulinia or stroke), cardiovascular diseases for heart failure applicable, but in a contraction or stroke).
                                                                                                                                                             25-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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239; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                        2000WO-EP09584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder
99EP-0203140.
99NL-1013140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coupled receptor; IGS4; IGS4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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99.6%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGS4B; schizophrenia;
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Amino acid

(first entry)

AAB67805 standard;

Protein;

nervous system disorder; psychiatric episodic paroxysmal anxiety; phobia;

Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia;

disorder;
migraine;

Parkinson's disease; epilepsy; bulimia; stroke;

sequence of G-protein coupled receptor IGS4B short version

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Вр Q B QΥ Вb QYВþ Ş

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RESULT 6
AAB67805
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                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               These diseases include peripheral nervous system, psychiatric and central cancerdate type phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, cmyocardial infarction or hypertension), dyslipidemias, obesity, emesis, cardiovascular diseases (e.g. heart failure, angina pectoris, cmyocardial infarction or hypertension), dyslipidemias, obesity, emesis, castorintestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammatory bowel disease or motility consists, or steoporosis, inflammatory bowel disease or motility consists, or steoporosis, inflammatory bowel disease or motility consists, or steoporosis, inflammatory bowel disease or motility consists or systems, or viral), pain, cancers, immune disorders, allergies, ceptical or ynecological disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal cystem, cardiovascular system, skeletal muscle, thyroid, lung or central and peripheral nervous systems, disorders the rest of the gastrointestinal cystem, cardiovascular system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, vor overexpression or altered expression of IGS4.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New G-protein coupled receptors and useful for preventing, ameliorating disorders, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 81-82; 102pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or cancers
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31-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                1 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60
                                                                                                                                                                       ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLDNTS 180
                                                                      VLVCLVILOHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT 120
                                                                                                                                                    ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                   VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000US-0222047
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                                                                                                                                                                                                                                                                                                                                                                                            Score 1252; DB 22;
Pred. No. 4.4e-141;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loeken C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the polynucleotides encoding or correcting nervous system dyslipidemias, inflammations,
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                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Query Match
Best Local S
Matches 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the short version of a human G-protein coupled receptor designated IGS4B. IGS4 exists in two polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for preventing, ameliorating disorders, cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overexpression or altered expression of IGS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New G-protein coupled receptors and the polynucleotides encoding tuseful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deleersnijder W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200125269-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2001
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                               IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                                                  ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                         VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLEGPVGCYFKT 120
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                                                                                   ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                          VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKT
                                                                                                                                                                                                                                                                                                         MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
AAF80325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
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99NL-1013140.
2000EP-0202683.
2000US-0222047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1252; DB 22; Pred. No. 4.4e-141;
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28-MAY-1999;
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12-MAR-1999;
12-MAR-1999;
     The present amino acid sequence is the hRUP6, an endogenous human orphan 6 protein-coupled receptor (GPCR). The full length hRUP6 cDNA was cloned by RT-PCR using human thymus cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands, and to screen jedentified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue
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28-MAY-1
29-JUN-1
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29-SEP-1
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99US-0120416.
99US-0121852.
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                                                                                                                                                                                                                                                                                                                                                                       Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical;
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12-NOV-1998;
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27-NOV-1998;
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PHARM
                  99US-0141448.
99US-0151114.
99US-0152524.
99US-0156633.
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99US-0156634.
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Pred. No. 4.5e-141;
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Best Local Similarity
Matches 239; Conserv
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                        Ahmad
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(ASTR ) ASTRA
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DB; AAA46022.
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                     J,
                                                                        AB.
                                                                                                PHARMA INC
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                     O'Donnell
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Pred. No. 4.5e-141;
1; Mismatches 0;
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RESULT 10
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24-FEB-2000; 2000JP-0052252.
30-MAR-2000; 2000JP-0097896.
19-JUN-2000; 2000JP-0187536.
                                                                                                                                                                                                                               Homo
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                       WPI; 2001-488917/53.
N-PSDB; AAH43072.
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                                                                                                                                                                                                                                                                                                                                      AAG63353 standard;
  Identifying
                                                                   Hinuma
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Pred. No. 4.5e-141;
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Best Local :
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24 - FEB - 2000;
30 - MAR - 2000;
19 - JUN - 2000;
      Identifying predicted or actual structures of two chemical or physical library by mass spectrometry correlating molecular mass measurements of two or shared chemical history -
                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of binding properties of neuromedin U to TGR-1. The method is useful for screening preventatives and remedies for hypertension, stress diseases, etc.. TGR-1 antagonists are also useful for treating the same diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemical or physical library by mass spectrometry comprising correlating molecular mass measurements of two or more members with shared chemical history - \,
                                                              N-PSDB;
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                                                              2001-488917/53.
)B; AAH43075.
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1.5e-141;
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                    more
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RESULT 12
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Best Local
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31-MAR-2000;
23-MAY-2000;
               The
                                                                     genes
with
triphosphate (GTP)-binding protein-coupled receptor.
                                           Claim
                                                                              Family of guanosine triphosphate binding protein genes encoding them for treatment and prevention
                                                                                                                          N-PSDB;
                                                                                                                                                                  Matsumoto S, Sugiyama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of binding properties of neuromedin U to TGR-1. The method is useful for screening preventatives and remedies for hypertension, stress diseases, etc.. TGR-1 antagonists are also useful for treating the same diseases.
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                                                                                                                                       2001-425663/45
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                                                                      these receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
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                                        1; Pages 100-103; 137pp; Japanese
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                                                                                                                                                                                                                                  ; 99JP-0375152.
; 2000JP-0101339.
; 2000JP-0155978.
                                                                                                                                                                                                                                                                                                                                                                                                         protein-coupled receptor; neuroprotective; immunomodulatory;
rinary; circulatory; anorectic; human; guanosine triphosphate;
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               is
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               protein sequence
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Pred. No. 4.5e
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. No. 4.5e-141;
ismatches 0;
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                                                                                                                                                                             Yoshida
              for a human
                                                                                coupled receptors and of diseases associated
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RESULT 13
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                                                                                                                                                                                                                                                                                                                         Human; G-protein coupled receptor; SNORF72; neuromedin U neuropeptide; NNU; inflammation; arrhritis; autoimmune disease; septicaemia; psychotic; mental retardation; transplant rejection; neurological disorder; anxiety; respiratory disorder; depression; schizophrenia; dementia; obesity; pain; gastrointestinal disorder; hypertension; hypotension; epilepsy; diabetes; ischaemia; stroke; cancer; sexual disorder; circadian disorder; anorexia; dermatological; psoriasis; Parkinson's disease; nausea; bulimia; allergy; Alzheimer's disease; AIDS; hormonal disorder; memory disorder; migraine; cardiovascular disorder; renal disorder; bone disease; delirium; asthma; cardiovascular disorder; renal disorder; bone disease; delirium; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for the investigation, diagnosis, treatment and prevention of diseases associated with GTP-binding protein-coupled receptors, including neurological, circulatory, digestive system, immune system, muscle and urrinary system disorders. GTP-binding proteins are also known as
                        WO200144297-A1
                                                                                                                 Domain
                                                                                                                                           Domain
                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                     Cushing's disease; dysmenorrhoea; antianginal; cytostatic; osteoporosis; metabolic disorder; behavioural disorder; Addison's disease; dyskinesia;
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                                                                                                                                                                                                                                                                                          tranquiliser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein coupled receptor, SNORF72.
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                                                                                                                                                                                                                                                                                          antiulcer; antiaddictive.
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                                                                                                                 /label=
215..240
                                                                /label=
301..33
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                                                                                                                                           166..179
                                                                                                     /label=
                                                                                                                                                        /label=
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                  /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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99.6%;
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Pred. No. 4.5e-141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human G-protein coupled receptors, SNORF62 and SNORF72 and their corresponding cDNA molecules. SNORF62 and SNORF72 creceptors are specific for neuromedin U (NMU) neuropetides, hence they are also known as NMU receptors. The agonist and antagonist of NMU receptors are useful for treating an abnormality in a subject that is alleviated by decreasing or increasing the activity of NMU receptor. The NMU receptors serves as a valuable tool for designing drugs which are useful for treating various pathophysiological conditions such as inflammation, arthritis, autoimmune diseases, transplant rejection, graft vs host disease, bacterial, fungal, protozoan and viral infections, septicaemia, AIDS, pain, psychotic and neurological disorders, including anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, neuromotor disorders, respiratory disorders, asthma, cating/body weight disorders including obesity, bulinia, diabetes, and disorders, ischaemia, stroke, cancers, sexual disorders, circadian disorders, renal disorders, troke, cancers, sexual disorders, circadian
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders, ischaemia, stroke, cancers, sexual disorders, circadian disorders, renal disorders, bone diseases including osteoporosis, benign prostatic hypertrophy, gastrointestinal disorders, nasal congestion, dermatological disorders such as psoriasis, allergies, parkinson's disease, Alzheimer's disease, acute heart failure, angina disorders, delirium and dyskinesias such as Huntington's disease. They can also be used to regulate steroid hormone disorders, epinephrine release disorders, electrolyte balance disorders, endocrine disorders, memory disorders, somatosensory disorders, metabolic disorders, behavioural
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A purified mammalian SNORF62 or SNORF72 receptor protein for identification of compounds to treat e.g. inflammation, arthritis, autoimmune diseases, transplant rejection, AIDS, cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 4; 256pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
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  184
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence
                                                                                                                                                         MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
                  IHGIKPHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                               ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                  ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS 180
                                                                                                                                                                                                                                                                              MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-390240/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                            so, drug addiction, migraine, Addison's disease, Cushing's prevent miscarriage, induce labour or to treat dysmenorrhoea ent sequence is human G-protein coupled receptor, SNORF72.
                                                                                                                                                                                                                                                                                                                                                                                                          415
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2000US-0558099.
2000US-0609146.
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                                                                                                                                                                                                                                                                                                                      Score 1252; DB 22;
Pred. No. 4.5e-141;
1; Mismatches 0;
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243
                                       240
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RESULT 14 AAB67802

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1 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPJFVVGVIGN 60 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 63

Matches

Conservative

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Query Match
Best Local Similarity
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                                                                                                                                                   These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardial infarction or hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal
                                                                                                          central and peripheral nervous systems, disorders of the gastrointestina system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, overexpression or altered expression of IGS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G-protein coupled receptors and the polynucleotides encoding useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobia; migraine; epilepsy; bulinia; stroke cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                  coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms. IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases.
                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deleersnijder W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gynecological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the long version of a human G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SOLV ) SOLVAY PHARM BV.
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DB; AAF80322.
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                                                                                415
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99NL-1013140.
2000EP-0202683.
2000US-0222047.
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                     99.1%;
99.6%;
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Score 1252; D
Pred. No. 4.5e
1; Mismatches
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DB 22;
4.5e-141;
hes 0;
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24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
           coupled receptor designated IGS4B. IGS4 exists in two polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's disease, migraine, epilepsy, bulimia or stroke), cardiovascular diseases (e.g. heart failure, angina pectoris, myocardalal infarction or hypertension), dyslipidemias, obesity, emesis gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammatory immune disorders, allergies, fundada, protozoan or viral), pain, cancers, immune disorders, allergies,
                                                                                                                                                                                                                                                        Claim 19; Page 85-86;
                                                                                                                                                                                                                                                                                                         New G-protein coupled receptors and the polynucleotides encoding them, useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations, pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety; phobla; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia; gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder; allergy; sepsis;
                                                                                                                                                                                                                 The present sequence represents the long version of a human G-protein
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gynecological disorders. Agonists
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; 99NL-1013140.
; 2000EP-0202683.
; 2000US-0222047.
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                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                overexpression or altered expression of IGS4.
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                IHGIKFHYFDNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                      ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS 180
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                                                                                                                                                                                                                                   MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 60
                                                                                                                                                                                                                 MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN 63
IHGIKFHYFPNGSLYPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
                                                                       ALFETYCFASILSITTYSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                          239;
                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                         99.1%;
99.6%;
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
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(without alignments)
567.428 Million cell updates/sec
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Compugen Ltd.
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                              hypothetical prote angiotensin II rec
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RESULT T15816

hypothetical protein C48C5.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Mar-2000

LIGNMENTS LIGNMENTS  LIGNMENTS  131-Dec-1991 #  ression of the ression of the famil as a hormone)  r: glycoproteir predicted <tm <tm="" <tm<="" predicted="" s="" th=""><th>Bes Mat</th><th>RESULT neurot C:Spec C:Dace C:Acce R:Tana Neuron A:Titl A:Refe A:Acce A:</th><th>. w w w w w w w w &amp; A A A A A A</th></tm>	Bes Mat	RESULT neurot C:Spec C:Dace C:Acce R:Tana Neuron A:Titl A:Refe A:Acce A:	. w w w w w w w w & A A A A A A
ext_change 17-Mar-2000 ext_change 17-Mar-2000 loned rat neurotensin II r of G protein-coupled ellular mediator in pe transmembrane protein > 5 6 6 7 # status predicted Length 424; Indels 12; Gaps AVSDLLVLLLGMPLEVY 101	cal similarity 35.1%; Pred. No. 1.3e-22; 72; Conservative 50; Mismatches 71; Indels 12; Ga 72; Conservative 50; Mismatches 71; Indels 12; Ga vsvvvpifvvgvignvLvcLvILQHQamkTPTNYYLFSLAVSDLLVLLLGMPLEVY i::::    :	ensin receptor - rat ies: Rattus norvegicus (Norway rat) ies: Rattus norvegicus (Norway rat) ies: Rattus norvegicus (Norway rat) pec-1991 #sequence_revision 31-Dec-1991 #text_change ssion: JH0164 ka, K; Masu, M; Nakanishi, S. 4, 847-854, 1990 e: Structure and functional expression of the cloned rat   rence number: JH0164; MUID:90297956; PMID:1894443 ssion: JH0164 cule type: mRNA cule type: mRNA dues: 1-424 < CTAN> neuromodulator in the brain and as a hormone) cellular menerianily: vertebrate rhodopsin ords: G protein-coupled receptor; glycoprotein; transmembrane #status predicted <tm2> 21/Domain: transmembrane #status predicted <tm3> 21/Domain: transmembrane #status predicted <tm4> 260/Domain: transmembrane #status predicted <tm4> 260/Domain: transmembrane #status predicted <tm5> 330/Domain: transmembrane #status predicted <tm5> 372/Domain: transmembrane #status predicted <tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm4></tm4></tm3></tm2>	ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotensin receptor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
C;Accession: S29506
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A;Accession: S29506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Cloning and expression of a complementary DNA encoding a high affinity human A; Reference number: $29506; MUID:93154505; PMID:8381365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad, M.; Gully, FEBS Lett. 317, 139-142, 1993
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A;Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1
C;Superfamily: adenosine receptor Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB37017.1; GSPDB:GN0A;Experimental source: strain Bristol N2; clone C48C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C48C5.
A;Reference number: Z18410
A;Accession: T15816
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R; Favello, A.
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       olecule type: mRNA
Residues: 1-418 <VIT>
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                112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 VGCYFKTALFETVCFASILSITTVSVERYVAILHP-FRAKLQSTRRRALRILGIVWGFSV 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 VVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QKHLNSTEEY---LAFLCGPRRSH-------
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                                                GTVGNTVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLTLLLAMPVELYNFIWVHHPWAF
                                                                                                                                        DPFQRAQAGLEEALLAPGFGNASGNASERVLAAPSSELDVNTDIYSKVLVTAVYLALFVV 76
                                                                                                                                                                                  DPFQKHLNSTEEYL------AFLCGPRRS-----HFFLPVSVVYVPIFVV 55
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      GPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVW 168
                                                                                            GVIGNVLVCLVILQH----QAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYE-MWRNYPFLF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLPMTVISVLYYLMALRVS 241
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                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                     25.8%;
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                                                                                                                                                                                                                                                   Score 325.5;
Pred. No. 1.7
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Pred. No. 3.6e-22;
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                         A; Molecule type: mRNA
A; Residues: 1-416 < CHA>
                                                                   A; Title: Molecular cloning of a levocabastine-sensitive A; Reference number: S68822; MUID:96228041; PMID:8647296 A; Accession: S68822
                                                                                                                                    R;Chalon, P.; Vita, N.; Kaghad, FEBS Lett. 386, 91-94, 1996
A;Cross-references: GB:X97121; NID:g1483579; PIDN:CAA65787.1;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: A88013
C; Accession: S68822
                                                               neurotensin receptor 2, levocabastine-sensitive -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein K10B4.4 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δã
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A; Residues: 1-418 <STO>
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                                                                                                                                                                                                                                                                                                                                          FERWLAICHPLRSKIFSTLWRANVLIILAWTISFVCALPIAFIVQINKLPLPEDAKYQPW
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                                                                                                                                                                                                                  ISVLYYLMALRV
                                                                                                                                                                                                                                                                                              --KFHYEP----NGSLVPGSAT-----CTVIKPMWIYNFIIQVTSF-LFYLLPMTV
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                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 303.5; DB 2
Pred. No. 1.6e-19;
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Guillemot,

M.; Bonnin,

neurotensin binding site J.; Delpech,

В.;

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PID:g1483580

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A;Cross-references: GB:M55533
A;Cross-references: GB:M55533
A;Note: the authors translated the codon CTT for residue 213 as Ala, GTG C;Genetics:
A;Gene: FlyBase:5-HT7
A;Cross-references: FlyBase:FBgn0004573
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: hypothalamus C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane pr F;33-58/Domain: transmembrane #status predicted <TM1>F;70-91/Domain: transmembrane #status predicted <TM2>F;110-131/Domain: transmembrane #status predicted <TM3>F:155-175/Domain: transmembrane #status predicted <TM4>F;204-230/Domain: transmembrane #status predicted <TM5>F:296-315/Domain: transmembrane #status predicted <TM6>F;335-361/Domain: transmembrane #status predicted <TM6>F;335-361/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serotonin receptor 7 - fruit fly (Drosophila melanogaster)
(Alternate names: 5-hydroxytryptamine receptor 7 (5-HTR7)
C;Species: Drosophila melanogaster
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Accession: A38271
R;Witz, P.; Amlalky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990
A;Title: Cloning and characterization of a Drosophila serotonin receptor tha
;Reference number: A38271; MUID:91062395; PMID:2174167
;Accession: A38271
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Best Local
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Best Local
314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TALYSLIFAFGTAGNALSVHVVLKARAGRPGRLRYHVLSLALSALLLLLLVSMPMELYNFV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
CTVCQ---
                                       CTVIKPMWIYNFIIQVTSFL--FYLLPMTVISVLYY
                                                                                RYLAITKPLEYGVKRTPRRMMLCVGIVWLAAACISLPPLLILGNE-HEDEEGQPI-----
                                                                                                                          RYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSAT 200
                                                                                                                                                                           ALSDLCVALLVMPMALLYEVLEKWN-----FGPLLCDIWVSFDVLCCTASILNLCAISVD
                                                                                                                                                                                                    AVSDLLVLLLGMPL----EVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVE 140
                                                                                                                                                                                                                                                                                                     EEYLA--FLCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFYLLPMTVISVL----YYLMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRLLSLVWVASLGLALPMAVIMGQKHEVESADGEPEPASRVCTVLVSRATLQVFIQVNVL 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSHYPWVFGDLGCRGYYF---VRELCAYATVLSVASLSAERCLAVCQPLRARRLLTPRRT 152
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35.3%;
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Pred. No. 1.6e-17;
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Pred. No. 2
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nes 73;
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                                       234
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                                                                                                                                                                                                                                                                                                                                                                                             Length 564;
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A;Cross:Telectonics: Control of A;Cross:Telectonics: Control of A;Crinnama, S.; Hosoya, M.; Ogi, K.; Tanaka, H.; Nagai, Y.; Biochim. Biophys. Acta 1219, 251-259, 1994
A;Title: Molecular cloning and functional expression of a A;Title: Molecular cloning and functional expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thyrotropin-releasing hormone receptor - human
(;Specles: Homo sapiens (man)
(;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
(;Accession: $40682; JN0759; $50151; $50152; I38356; JN0708
R;Matre, V.; Karlsen, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen,
Biochem. Biophys. Res. Commun. 195, 19-185, 1993
A;Title: Molecular cloning of a functional human thyrotropin-releasing hormone recept A;Reference number: $40682; MUID:93371401; PMID:8395824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M59811; GB:M37490; NID:g202153; PIDN:AAA40480.1; PID:g202154 C;Superfamily: adenosine receptor Al C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Straub, R.E.; Frech, G.C.; Joho, R.H.; Gershengorn, M.C. Proc. Natl. Acad. Sci. U.S.A. 87, 9514-9518, 1990 A;Title: Expression cloning of a cDNA encoding the mouse pituitary A;Reference number: A39251; MUID:91088548; PMID:2175902 A;Accession: A39251 A;Molecule type: mRNA A;Residues: 1-393 <STR>
                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X75071; NID:g404157; PIDN:CAA52965.1; PID:g404158 R;Yamada, M.; Monden, T.; Satch, T.; Satch, N.; Murakami, M.; Iriuchijima, Biochem. Biophys. Res. Commun. 195, 737-745, 1993 A;Title: Pituitary adenomas of patients with acromegaly express thyrotroping.
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A; Residues: 1-398 < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: S40682
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C;Accession: A39251
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C; Species: Mus musculus (house mouse)
                                                                                                  A;Cross-references: GB:D16845; NID:g577631; PIDN:BAA04120.1; PID:g577632 R;Hinuma, S.; Hosoya, M.; Ogi, K.; Tanaka, H.; Nagai, Y.; Onda, H.
                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-398 < YAM>
                                                                                                                                                                                                                   A; Reference number: JN0759; MUID:93384596; PMID:8396925 A; Accession: JN0759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATVLYGFIA. 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CMLWFFLLDLNISTYKNAVVV----SCGYKISRNYYSPIYLMDFGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDSIYGSW-----VYGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISVLYYLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIY
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72; Conserv
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                                    human thyrotropin-releasing
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                                                                                                                                                                                                                                                                                                         thyrotropin-releasing
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                                                                                                                     A;Cross-references: GB:S60053; NID:g300151; PIDN:AAB26491.1; PID:g300152 C;Superfamily: adenosine receptor A1
                                                                                                                                                                                                                                          J. Mol. Endocrinol. 10, 199-206, 1993
A; Title: Functional expression and molecular characterization of the thyrotrophin-releas A; Reference number: I56444; MUID:93249585; PMID:8387312
                                                                                                                                                                                                                         A; Reference number: A; Accession: I56444
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                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                   A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                             R; Sellar, R.E.; Taylor, P.L.; Lamb, R.F.; Zabavnik, J.; Anderson, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЪ
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A;Map position: 8q23-8q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MR; Duthie, S.M.; Taylor, P.L.; Anderson, L.; Cook, J.; Ei Mol. Cell. Endocrinol 95, R1-R15, 1993
A;Title: Cloning and functional characterisation of the A;Reference number: 138356; MUID:94063224; PMID:8243797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 267-398 <HI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <HI
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X72089; NID:g440155; PIDN:CAA50979.1; PID:g440156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-398 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I38356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S50152
                                           Matches
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194-215/Domain: transmembrane 267-288/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :146-168/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;29-51/Domain: transmembrane #status predicted;62-83/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: GDB:TRHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                        Accession: I56444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297-319/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                pecies: Mus sp. (mouse)
Date: 26-Jul_1996 #sequence_revision 26-Jul-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                             rotrophin-releasing hormone receptor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
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      15
                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .21/Domain: transmembrane #status
LEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVV----GVIGNVLVCLVILQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATC----TVIKPMWIYNFI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSVVYVPIFV-VGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLL-LGMPL---E 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V----FYVVPMILATVLYGFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQVTSFLFYLLPMTVISVLYYLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYGSW-----VYGYVGCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTILLVLIICGLGIVGNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDS 86
                                           Conser 72;
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                                         Conservative
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                                                         20.4%;
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                                           49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #status predicted
                                    Score 258; DB
Pred. No. 1.8e
#9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 259;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                   GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L.; Cook, J.; Eidne, K.A.
                                       DB 2; :
L.8e-15;
hes 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <TM7>
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                                       Indels
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                                       36;
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                                  Gaps
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F;32-54/Domain: transmembrane #status predicted <TM2>F;71-92/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                               F; 1-22/Domain:
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                                                                                                                                                                                                                                                                                A:Note: the authors translated the codon ACA for residue 88\ as C:Superfamily: adenosine receptor Al
                                                                                                                                                                                                                                                                                                                                          A;Residues: 30-58,'P',60-222,'T',224
A;Experimental source: strain Wister
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 30-58, 'P', 60-222, 'T', 224-261 <YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Yamada, M.; Monden, T.; Satoh, T.; IIzuka, M.; Murakami, M.; Iriuchijima, T.; Mori, Biochem. Biophys. Res. Commun. 184, 367-372, 1992
A;Title: Differential regulation of thyrotropin-releasing hormone receptor mRNA level A;Reference number: PQ0326; MUID:92231953; PMID:1373613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: GH cells
A;Experimental source: GH cells
A;Note: sequence extracted from NCBI backbone (NCBIN:104788, NCBIP:104795)
A;Note: sequence extracted from NCBI backbone (NCBIN:104788, NCBIP:104795)
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A:Residues: 1-12,'D',14-290,'K',292-412 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:D17469; NID:g464199; PIDN:BAA04289.1; PID:g464200 R;Zhao, D.; Yang, J.; Jones, K.E.; Gerald, C.; Suzuki, Y.; Hogan, P.G.; Chin, W.W.; T. Endocrinology 130, 3529-3536, 1992 A;Title: Molecular cloning of a complementary deoxyribonucleic acid encoding the thyr A;Reference number: A49168; MUID:92283212; PMID:1317787 A;Accession: A49168
                                                                                                              F;165-186/Domain: transmembrane #status predicted <TM5>
                                                                                                                                              F;116-140/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: PQ0326
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A;Title: Cloning and expression of the thyrotropin-releasing A;Reference number: S23436; MUID:92322017; PMID:1377915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995  #sequence_revision 13-Jan-1995  #text_change 11-Jan-2000
C;Accession: S23436; I53279; A49168; PQ0326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: I53279
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Reference number: I53279; MUID: 94102223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X64630; NID:g57394; PIDN:CAA45913.1; R;Kimura, N.; Arai, K.; Sahara, Y.; Suzuki, H.; Kimura, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-412 <PEN>
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     Matches
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     Local Similarity
nes 72; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHMRTATNCYLVSLAVADLMVLVAAGLPNITDSIYGSW-----VYGYVGCLCITYLQYLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENETVSELNQTEL - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-412 <RES>
                                                                                                                                                                                                                               transmembrane #status predicted <TM1>
        Conservative
                                                                                                                                              transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , K.; Sahara,
432-440, 1994
                                  20.4%;
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     49;
                 Score 258; Db 2,
No. 1.8e-15;
  Mismatches
                                                                                                                                           predicted
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     ; 08
                                                    Length 412,
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  Indels
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  36;
Gaps
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GH

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oploid receptor mu variant MORIA - human
C:Species: Homo sapiens (man)
C:Date: 12-Uul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: S65693; S51216
R;Bare, L.A.; Mansson, E.; Yang, D.
submitted to the EMBL Data Library July 1994
A;Description: Expression of two variants of the human mu opioid receptor minimum for the human mu opioid rec
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C:Species: Cavia porcellus (guinea pig)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Apr-2000
C:Accession: I56595
R:Aharony, D.; Little, J.; Thomas, C.; Powell, S.; Downey-Jones, M.; Graham, J. Recept. Res. 14, 399-421, 1994
A;Title: Isolation and characterization of neurokinin A receptor cDNAs from 9A:Reference number: I56595; MUID:95182423; PMID:7877137
A;Accession: I56595
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-402 <RES>
A;Cross-references: GB:S76253; NID:g913274; PIDN:AAB33553.1; PID:g913275
C;Superfamily: neurokinin 1 receptor
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A;Title: Expression of two variants of the human mu opioid A;Reference number: S51215; MUID:95046336; PMID:7957926 A;Accession: S51216 A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 -VIGGIWLVALALAFPQC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVTSFLFYLLPMTVISVLYYLMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVI-----KPMWIYNFII 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMWRNYPELEGPVGCYEKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFASILSITTVSVERYVAILHPFRAKLOSTRRRALRILGIVWGFSVLFSLPNTSIHGIKF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IV---LIYLLPLTVMFVAYSIIGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STYKDAIVI ---- SCGYKISRNYYSPIYLMDFGV ----- FYVMPMILATVLYGFIA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYFPNGSLVPGSATC-----TVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INASSCSITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWAFTSIYCMLWFFLLDLNI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHMRTATNCYLVSLAVADLMYLVAAGLPNITDSIYGSW-----VYGYVGCLCITYLQYLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAMKTPTNYYLFSLAVSDLLVLL-LGMPL---EVYEMWRNYPFLFGPVGCYFKTALFETV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MENETVSELNQTEL - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 59; Conserv
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Pred. No. 1.9e-15;
5; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
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A;Residues: 1-398 <- ROS>
A;Cross-references: EMBL:U26915; NID:g1055230;
A;Note: the nucleotide sequence was submitted C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C.Accession: A57510; 146665; S66513; I49300
R;Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, J. Biol. Chem. 270, 15877-15883, 1995
A;Title: Characterization of the murine mu opioid receptor gene.
A;Reference number: A57510; MUID:95318184; PMID:7797593
                                                                            C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G
                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U10561; NID:g555696; PIDN:AAB60673.1; R;Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W. FEBS Lett. 369, 192-196, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A;Title: Genomic structure analysis of promoter sequence of a A;Reference number: I48665; MUID:94377496; PMID:8090773
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                                                                                                                                                                                                                                                                                                         A; Title: Antisense mapping the MOR-1 opioid receptor: evidence A; Reference number: 149300; MUID:95377399; PMID:7649256
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-398 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mu opioid receptor -
                                                                                                                       A; Introns:
                                                                                                                                             A; Gene: MOR-1
                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                       A; Accession: S66513
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
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  Matches
                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVISVLYYLMALRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSAIGLPVMFIATTKYR-----QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVI--KPMWIYNFIIQVTSFLF-YLLPM
                                                                                                                       95/2; 213/1; 386/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-398 <KAU>
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                     Similarity
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  Conservative
                                                                                                                                                                                 EMBL:U26915; NID:g1055230; PIDN:AAA81170.1; PID:g1055231 ide sequence was submitted to the EMBL Data Library, Nove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse
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                   20.2%;
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28.7%;
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  42;
Score 255; DB Pred. No. 3.1e 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 255.5;
Pred. No. 2.
                                                                            protein-coupled receptor; glycoprotein;
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                 3.1e-J
DB 2; 1
3.1e-15;
nes 84;
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                                      Length 398
                                                                                                                                                                                 EMBL Data Library, November 1995
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  32;
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34 CGPRR----SHFFLP-----

--- VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTP

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C.Keywords: G protein-coupled receptor; glycoprotein; tra
F;73-96/Domain: transmembrane #status predicted <TMM1>
F;107-132/Domain: transmembrane #status predicted <TMM2>
F;144-165/Domain: transmembrane #status predicted <TMM3>
F;188-208/Domain: transmembrane #status predicted <TMM4>
                                                                   F;283-304/Domain: transmembrane *status predicted <TMM6> F;323-342/Domain: transmembrane *status predicted <TMM7> F:9,12,33,40,48/Binding site: carbohydrate (Asn) (covale)
                                                                                                                                               F;188-208/Domain: transmembrane *status predicted <TMM4> F;236-257/Domain: transmembrane *status predicted <TMM5>
                                                                                                                                                                                                                                                                                                       A; Map position: 6q24-6q25
C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:137216; OMIM:600018
                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: OPRM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-50,'N',52-233,'V',235-400 <WAN>
A;Cross-references: GB:L25119; NID:g452072; PIDN:AAA20580.1
R;Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A38991
A;Accession: A38991
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L29301; NID:g459831; R;Wang, J.B.; Johnson, P.S.; Persico, A.M.; submitted to GenBank, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number:
A; Accession: S51215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Expression of two variants of the A; Reference number: S51215; MUID: 95046336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-50,'N',52-400 <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S41075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterizat. A;Reference number: S41075; MUID:94139928; PMID:7905839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-400 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Mestek, A.; Hurley, J.H.; Bye, L.S.; Campbell, A.D.; Chen, Y.; Tian, M.; Liu, J. Neurosci. 15, 2396-2406, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: MOR1 protein; opioid receptor mu C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000 C;Accession: I56553; A38991; S41075; S51215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bare, L.A.; Mansson, E.; Ya
BS Lett. 354, 213-216, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                               Rtatus: preliminary nolecule type: mRNA Residues: 387-400 <BAR>
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  Local Similarity
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20.1%;
28.3%;
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Score
Pred.
253.
4.3e-15;
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                                                                      (covalent) #status
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                       Length 400
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A; Map pusser

A; Introns: #status absent
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; horn
C; Keywords: G protein-coupled receptor; glycoprotein; horn
F; 44-69/Domain: transmembrane #status predicted <TM1>
F; 80-105/Domain: transmembrane #status predicted <TM3>
F; 117-138/Domain: transmembrane #status predicted <TM4>
F: 158-180/Domain: transmembrane #status predicted <TM4>
F: 158-180/Domain: transmembrane #status predicted <TM5>
F: 158-180/Domain: transmembrane #status predicted <TM5
                                                                                                                                                                                                                                                                                                                                                                                                                                              F;254-281/Domain: transmembrane #status predicted <TMG>
F;288-315/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status F;115-193/Disulfide bonds: #status predicted F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kin F;328/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, ramada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S. Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A; Title: Cloning and functional characterization of a family of human and mouse somat A; Reference number: A41795; MUID:92108031; PMID:1346068
A; Accession: B41795
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A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Residues: 1-369 <YAM>
A;Cross-references: GB:M81830; NID:g307435; PIDN:AAA58248.1;
A;Cross-reference extracted from NCBI backbone (NCBIN:74769, )
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A; Introns: #status absent
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LAVVHPIKSAKWRRPRTAKMITMAVWGVSLLVILPIMIYAGLRSNQW---
                                                                                                                                                                    LAVSDLLVLLLGMP-LEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERY
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                                                                                                                                                                                                                                                                                   NSTEEYLAFICGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFS
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NCBIP:74770)
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 17, 2003, 02:39:56; Search time 23 Seconds (without alignments)
436.403 Million cell updates/sec

Title: US-09-684-725-2

Perfect score: 1263
1 MEKLQNASWIYQOKLEDPFQ......LLPMTVISVLYYLMALRVSI 242

Pering table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

## SUMMARIES

Result		9 Ouerv				Ç.
No.	re	Match	Length	BB	ID	cription
ш	338	œ		1	NTR1_RAT	P20789 rattus norv
2	333	26.4	412	1	í i	3 homo sa
ω		26.3	424	_		mus m
4	325.5	25.8	418	_	NTR1_HUMAN	9 home
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7	277	•	366	سر	GHSR_HUMAN	
- σο	274	٠	364	_	GHSR_RAT	rattu
9		21.7	366	_	GHSR_PIG	sus sc
10	270.5	•	395	$\vdash$	TRFR_CHICK	gall
11	268	21.2	257	$\vdash$	GHSR_MOUSE	
12	265	•	393	_	TRFR_MOUSE	mus m
13	259	20.5	398	-	TRFR_HUMAN	P34981 homo sapien
14	258	20.4	398	_	TRFR_BOVIN	t sod
15	258	20.4	398		TRFR_SHEEP	Q28596 ovis aries
1 E	8.52	20.4	4 1 O		NTR2_HUMAN	095665 homo sapien
17	١.,	20.4	412	· _	TRFR_RAT	rattu
18		20.4	400	_	OPRM_MACMU	Q9myw9 macaca mula
19	57.	٠	402	Н	NK2R_CAVPO	Q64077 cavia porce
20	56.	٠	401	_	OPRM_BOVIN	bos ta
21	25	•	398	Н	OPRM_MOUSE	P42866 mus musculu
22			400	ب	OPRM_HUMAN	home
23	253	20.0	417	٢	NTR2_MOUSE	mus π
24	. 2	•	369	ш	SSR2_HUMAN	home
25		٠	401	<b></b>	OPRM_PIG	sus s
26			460	_	OX2R_RAT	P56719 rattus norv
27	24		369	<u>, , , , , , , , , , , , , , , , , , , </u>	SRZ	sus
28	247.5		368	ᆫ	SSR2_BOVIN	sod
29	7		369	٠,	SSR2_RAT	P30680 rattus norv
30	Ģ		370	_	OPRX_CAVPO	cavia p
31	·	19.3	384	ᆫ	NK2R_MOUSE	mus mu
32	2	19.2	363	_	SSR5_RAT	P30938 rattus norv
3.3		19.2	385	,_	NK3R_MOUSE	P47937 mus musculu

241.5 19.1 384 1 NK2R_BOVIN 241.5 19.1 384 1 OX2R_CANFA 241.5 19.1 444 1 OX2R_CANFA 241.5 19.1 444 1 OX2R_CANFA 240.5 19.0 442 1 D2D_XENLA 240.5 19.0 442 1 D2D_XENLA 240.5 19.0 359 1 AG2R_BOUSE 240 19.0 359 1 AG2R_DIG 240 19.0 359 1 AG2R_DIG 240 19.0 359 1 AG2R_RAT	19.1 384 19.1 384 19.1 359 119.0 442 119.0 442 119.0 359 119.0 359	45	44	43	42	41	40	39	38	37	36	35	34
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	1 NKZR BOVIN P05363 1 NKZR BOVIN P05363 1 OXZR_CANFA Q9tup7 1 AGZR_BOVIN P25164 1 DZDL_XENLA Q4628 1 OXZR_HUMAN Q44628 1 OXZR_HUMAN Q43614 1 AGZR_MOUSE P29754 1 AGZR_PIG P30555 1 AGZR_RAGT P297552 1 AGZR_RAGT P297552 1 AGZR_RABIT Q97512	19.0	19.0	19.0	19.0	19.0	19.0	19.0	19.0	19.1	19.1	19.1	7.67
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	P03333 P05363 P051047 P25104 P24628 O43614 O43614 P29754 P30555 P29754 P25095 P27512	NK3R_RABIT	AG2S_MOUSE	AG2R_RAT	AG2R_PIG	AG2R_MOUSE	AG2R_CAVPO	OX2R_HUMAN	D2D1_XENLA	AG2R_BOVIN	OX2R_CANFA	NK2R_BOVIN	CTKM_KAT

## ALIGNMENTS

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HYKININS RECEPTORS. 44 46 46 46 46 47 47 48 48 49 41 47 49 49 49 40 40 40 40 40 40 40 40 40 40 40 40 40	RAT STANDARD; PRT; 424 AA. 89; EB-1991 (Rel. 17, Created) EB-1991 (Rel. 17, Last sequence update) UL-1998 (Rel. 36, Last annotation update) otensin receptor type 1 (NT-R-1) (High-af. nsitive neurotensin receptor) (NTRH).  1. 1. 1. 2. 2. 2. 2. 2. 2. 2. 3. 3. 3. 3. 3. 3. 3. 3. 3. 4. 3. 4. 4. 4. 4. 5. 4. 4. 5. 4. 5. 4. 5. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.
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	finity  prata;  pridae;  pridae;  neuror  neuror  neuror  neuror  neuror  cotein.
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Best Local :
 Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D., Tan C.P., Mckee K.K., Pong S.-S., Griffin P.R., Howard A.D.; "Growth hormone secretagogue receptor family members and ligands." Endocrine 14:9-14(2001).

-!- FUNCTION: Receptor for motilin.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk I
Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri
Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.
O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A.,
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM A).

MEDLINE-98110578; pubMed=9441746;

MCKGE K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,

Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;

"Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors.";

Genomics 46:426-434(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
LIPID
                                                                          MEDLINE=21219832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Motilin receptor (G protein-coupled receptor MTLR1 OR MTLR OR GPR38.
                                                                                                                                            SEQUENCE
                                                                                                                  Submitted
                                                                                                                                                                    Science
                                                                                                                                                                               system
                                                                                                                                                                                                                                                                    MEDLINE=99316084; PubMed=10381885;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                          Howard A.D.;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTLR_HUMAN
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                                                                                                                                                                                            for
                                                                                                                 (DEC-2000)
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424 AA;
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                                                                                                                                          N.A.
                                                                                                                                                                                            motilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
42
225
388
47054 .
                                                                           PubMed=11322507;
                                                                                                                                                                                                                                                                                   (ISOFORMS A AND
                                                                                                                                          (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Ve
Primates; Catarrhini;
                                                                                                                 to the EMBL/GenBank/DDBJ
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35.1%;
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Integral
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Pred. No. 1
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membrane
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AF8D9BCD3 CRC64;
                                                                                                                                                                                          human
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.2e-17
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                                                                                                                 databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
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Best Local
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DISULFID
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PRINTS; PR00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2;
Transmembra
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF034632; AAC26081.1; EMBL; AL137000; CAC19107.1;
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-i- TISSUE SPECIFICITY: EXPRESSED ONLY IN THYROID, STOMAC
                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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 LYYLM
                                                                                                                   LGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKL 153
                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                          PMWI - -
                                                                                 QSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPG-----
                                                                                                                                               CSPFPLGALVPVTAVCLCLFVVGVSGNVVTVMLIGRYRDMRTTTNLYLGSMAVSDLLI-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602885
                   PLWLSRAPPPSSPFSGPETAEAAALFSRECRPSPAQLGALRVMLWVTTAYFF-LPFLCLSI
                                                            LVTRRRVRALIAVLWAVALLSAGPFLFLVGVE--QDPGISVVPGLNGTARIASSPLASSP
                                                                                                      LGLPFDLYRLWRSRPWVFGPLLCRLSLYVGEGCTYATLLHMTALSVERYLAICRPLRARV 148
                                                                                                                                                                                         78;
                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                   412 AA;
                                                                                                                                                                                           Conservative
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358
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31.8%;
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Pred. No. 2.7e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL)
CYTOPLASMIC (1
2 (POTENTIAL)
                                                                                                                                                                                                                                  (IN ISOFORM B).
C13FF6165012DEF3 CRC64;
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N-LINKED (GLCNAC. . .) (POTENTIAL).

LVVVLAFIICWLPFHVGRIIYINTEDSRMMYESQYFNIVAL

QLFYLSASINPILYNLISKKYRAAAFKLLLAKKSRPRGFHR

SRDTAGEVAGDTGGDTVGYTETSANVKIMG -> RKWSRRG

SKDACLQSAPPGTAQTLGPLPLLAQLWAPLPAPFPISIPAS
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CYTOPLASMIC (
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6 (POTENTIA:
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4 (POTENTIAL
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3 (POTENTIAL).
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                                       -YNFIIQVTSFLFYLLPMTVISV 231
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                                                                                 SATCTVIK
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Query Match

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DOMAIN
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PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01479; NEUROTENSINR.

PRINTS; PR01480; NEUROTENSNIR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snider J., Sano H., Ohta M.;

"Neurotensin receptor type 1.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN.

ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDY.

CALCIUM SECOND MESSENGER SYSTEN.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED R:

HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _MOUSE
NTR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O88319;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD, MGI:97386, Ntsr.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003985, WTl_rec.
InterPro; IPR003984, WT_rec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97386; Ntsr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    SEQUENCE
                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                 Chordata;
Rodentia;
    47216
    X
X
                      N-LINKED (GLC)
BY SIMILARITY.
PALMITATE (PO)
                                                    N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL)
                                                                                                                                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                      CYTOPLASMIC (
6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (P
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmitate.
LMITATE (POTENTIAL).
8E9A723171A48711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                             (POTENTIAL).
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        밁
RA DeLoukas P., Matthews L. H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RC Coulson A., Coville G.J., Deadman R., Dahmi P.D., Dunn M.,
RC Coulson A., Coville G.J., Deadman R., Dahmi P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Mines S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Suce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTRI_HUMAN STANDARD; PRT; 418 AA.
P30989; Q9H4T5; Q9H4H1;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurotensin receptor type 1 (NT-R-1) (High-affinity levocabastine-insensitive neurotensin receptor) (NTRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and expression of a complementary DNA encoding a high affinity human neurotensin receptor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTSR1 OR NTKK.
HOmo sapiens (Human).
Homosapiens (Chordata; Chordata; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vita N., Laurent P., Lefort S., Chalon P., Dumont X., Kaghad
Gully D., le Fur G., Ferrara P., Caput D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93154505; PubMed=8381365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mman neurotensin receptor.";
317:139-142(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11780052
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Matches
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PRINTS; PR01480; NEUROTENSNIR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:8039; NTSR1.
MIM; 162651; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR003985; NT1_rec.
InterPro; IPR003984; NT_rec.
Pfam; PF00001; 7tm_1; 2.
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HSSP; P02699; 1F88.
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO TACHYKININS RECEPTORS.
GPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence and core 414:865-871(2001
                                                                     GTVGNTVTAFTLARKKSLQSLQSTVHYHLGSLALSDLLTLLLAMPVELYNFIWVHHPWAF
                                                                                                               GVIGNVLVCLVILQH--
                                                                                                                                                           DPFQRAQAGLEEALLAPGFGNASGNASERVLAAPSSELDVNTDIYSKVLVTAVYLALFVV
                                                                                                                                                                                                     DPFQKHLNSTEEYL------AFLCGPRRS------HFFLPVSVVYVPIFVV 55
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                         368
4
37
41
141
141
383
200
418 /
                                                                                                                                                                                                                                                   Conservative
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235
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96
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                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                      25.8%;
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                                                                                                               -QAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYE-MWRNYPFLF 111
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                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 (POTENTIAL).
CYTOPLASMIC (F
                                                                                                                                                                                                                                                                                                                                                              PALMITATE (POTENTIAL).
T -> A (IN REF. 2).
                                                                                                                                                                                                                                                                      Score 325.5;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC (
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5 (POTENTIAL).
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1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      .3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHATIDYLINOSITOL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                           Length 418;
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                   53;
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                                                                                                                                                                                                                                               Gaps
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RESULT 5
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Q63384;
01-NOV-1997
                                                                                                                                                                                                      PROSITE; pS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; pS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;

DOMAIN 1 32 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X97121; CAA65787.1; -
InterPro; IPR003986; GPCR_Rhodpsn.
InterPro; IPR003986; NT2_rec.
InterPro; IPR003984; NT_rec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chalon P., Vita N., Kaghad M., Guillemont M., Bonin J.,
Delpech B., le Fur G., Ferrara P., Caput D.;
"Molecular cloning of a levocabastine-sensitive neurotensin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Neurotensin receptor type 2 (NT-R-2) (High-affinity levocabastine-
                           TRANSMEM
                                                      DOMAIN
                                                                              TRANSMEM
                                                                                                                                  TRANSMEM
                                                                                                                                                             DOMAIN
                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                  PRINTS; PR01481; NEUROTENSN2R
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01479; NEUROTENSINR
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delpech B., le Fur
"Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTSR2 OR NTR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sensitive neurotensin receptor).
  DOMAIN
                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: EXPRESSED MAXIMALLY IN 7-DAY-OLD BRAIN AND EXPRESSION DECREASES PROGRESSIVELY UNTIL ADULTHOOD (35-DAY-OLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane TISSUE SPECIFICITY: ABUNDANT IN CORTEX LEVELS SEEN IN THE HEART AND INTESTINE TRANSPORTER FOR THE TENER TO THE TENER THE TENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S Lett. 386:91-94(1996).
FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASALLTVPMLFTMGEQNRSADGQH-----AGGLVCTPTIHTATV
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d receptor;
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                                                                                                                          1 (POTENTIAL).
CYTOPLASMIC (POTENT)
                        CYTOPLASMIC
4 (POTENTIAL
                                                                            EXTRACELLULAR 3 (POTENTIAL).
                             (POTENTIAL
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                                                (POTENTIAL).
                                                                                                                                                        (POTENTIAL).
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AND HYPOTHALAMUS,
                                                                                                                                                                                                         Lipoprotein; Palmitate. (POTENTIAL).
(POTENTIAL)
                                                                                                       (POTENTIAL)
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5HT1_DROME
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A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Bayenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Ferriag S., Fleischmann W.,
A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P20905; Q9VA21;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-hydroxytryptamine receptor 1 (5-HT receptor
5-HT7 OR 5HT-RI OR CG12073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
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DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                               Witz P., Amlaiky N., Plassat J.-L., Maroteaux L., Borrelli E., Hen R.; "Cloning and characterization of a Drosophila serotonin receptor that activates adenylate cyclase"; Proc. Natl. Acad. Sci. U.S.A. 87:8940-8944(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91062395; PubMed=2174167; Witz P., Amlaiky N., Plassat J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Oregon-R; TISSUE-Head;
                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5HT1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRILGIVWGFSVLFSLPNTSIHGIKFHY-FPNGSLVPGSATCTVIKPMWIYNFIIQVTSF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WRNYPFLFGPVGC---YFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVVYVPIFVVGVIGNVLVCLVILQHQAMKT-PTNYYLFSLAVSDLLVLLLGMPLEVYE-M 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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7 (POTENTIAL)
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PALMITATE (POTENTIAL)
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RA Harris N.L. Harvey D. Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L. Harvey D. Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McChed M.P., McPherson D.,
RA McIkulov G., Milshina N.V., Mobarry C., Morris J., Mschrefi A.,
RA McIkulov G., Milshina N.V., Mobarry C., Morris J., Mschrefi A.,
RA Meikolov J.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylses B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylses B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylses B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylses B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worrley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Shong W., Zhang G., Zhao Q., Zheng L.,
RA Yellon R., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Yellon R., Shong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Yellon R., Shong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Yellon R., Shong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Yellon R., Shong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
DOMAIN
DOMAIN
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; per00001; 7tm_l; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                 G-protein TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M55533; AAA28305.1; -
EMBL; AE003776; AAF57104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0004573; 5-HT7
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                                                                                                                                                                   DOMAIN
                                                                                                                                                                                    TRANSMEM
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COU
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165
189
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223
237
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331
455
477
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ĀΑ;
                                                                                                                                                                                                                                                                                                                                  receptor;
106
314
60861
                                                     188
198
222
236
236
258
278
302
330
353
454
476
476
564
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 X.
                                                                       EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                             Transmembrane;
0 (POTENTIAL)
                   ВҮ
                                  CYTOPLASMIC (POTENTIAL)
9 X 2 AA TANDEM DESCRIPTION
                                                                                                                                                                                                                                                         CYTOPLASMIC
2 (POTENTIA)
                                                                                                                                                                                  CYTOPLASMIC
4 (POTENTIAL
                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
                                                                                                                                                                                  (POTENTIAL
                                  X 2 AA TANDEM REPEATS OF
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                (POTENTIAL)
 0C8B9F8DA63D8095
                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF G-PROTEIN COUPLED
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                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               Glycoprotein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercial
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Query Match Best Local

Similarity

22.2%;

Score Pred.

DB 1;

Length 564;

Indels

28;

Gaps

9

.9e-1

Conservative

36;

Mismatches

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RESULT 7
GHSR_HUMAN
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                                                                                                                                MEDLINE-20067959; PubMed=10604470;
Kojima M., Hosoda H., Date Y., Nakazato
"Ghrelin is a growth-hormone-releasing a
                                                                                                                                                                                                                                               Smith
Tan C.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B)
MEDLINE=21255649; PubMed=11356716;
Petersenn S., Rasch A.C., Penshorn M.,
"Genomic structure and transcriptional
hormone secretagogue receptor.";
Endocrinology 142:2649-2659(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Howard A.D., Feighner S.D., Cully D.F., Arena J.P.,
Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,
Palyha O.C., Anderson J., Paress P.S., Diaz C., Chou M., Liu K.K.,
McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,
Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D
Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K
Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.,
A receptor in pituitary and hypothalamus that functions in growth
                                                                                                                         stomach.
                                                                                                                                                                                      FUNCTION
                                                                                                                                                                                                                         Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D., Tan C.P., Mckee K.K., Pong S.-S., Griffin P.R., Howard A.D., "Growth hormone secretagogue receptor family members and ligands."
                                                                                                                                                                                                                                                                         MEDLINE=21219832; PubMed=11322507;
                                                                                                                                                                                                                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                                                                                                                                                            hormone
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MEDLINE=96337998; PubMed=8688086;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
as well as non-peptide, low mol-
L-692,429, MK-0677, adenosine).
SUBCELLULAR LOCATION: Integral |
ALTERNATIVE PRODUCTS: 2 ISOFORM
                                          FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 protestimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and as well as non-peptide, low molecular weight secretagogues
                                                                                                                                                                                                                                                           R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTVIKPMWIYNFIIQVTSFL--FYLLPMTVISVLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTVCQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVSDLLVLLLGMPL----EVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFAAGEFVLPPLTSIF---VSIVLLIVILGTVVGNVLVCIAVCMVRKLRRPCNYLLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEYLA--FLCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSL
                                                                                                       402:656-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                        release.";
273:974-977(1996).
                                                                                                                                                                                                               14:9-14(2001).
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    ISOFORMS;
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 membrane protein MS; 1A (SHOWN HER!
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   HERE) AND
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Gupta S.K.,
   1B;
                                                           GHRP-6)
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                                             (e.g
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RESULT 8
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                     217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: SIMILARITY: BELONGS
                                                                                                                               QYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
                                                                                                                                                                       VTATCVALFVVGIAGNILTMLVVSRFRELRTTNLYLSSMAFSDLLIFLC-MPLDLVRLW
                                                                                                                                                                                           VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW
                                                                      IIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                      FVIWAVAFCSAGPIFVLVGVEHE---NGTDPWDTNECRPTEFAVRSGLLTVM--VWV---
                                                                                                            GIVWGFSVLFSLPNTSIHGIKFHYFPNGS----
                                                                                                                                                  RNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601898;
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                                                                                                                                                                                                                              Similarity
                                                  SSIFFFLPVFCLTVLYSLIGRKL
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366
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                                                                                                                                                                                                                                                            41328
                                                                                                                                                                                                                             31.7%;
                                                                                                                                                                                                                                       21.9%;
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TO FAMILY
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                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (
5 (POTENTIAL).
CYTOPLASMIC (PC
6 (POTENTIAL).
                                                                                                                                                                                                                          Score 277;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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CYTOPLASMIC (
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7 (POTENTIAL).
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1 OF G-PROTEIN C
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                                                                                                                                                                                                                 DB 1;
2.5e-13;
les 69;
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                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                            -LVPGSATCTVIKPMWIYNF
                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                           .) (POTENTIAL).
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DOMAIN
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth hormone secretagogue receptor type 1 (
                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               EMBL; AB001982; BAA21777.1; ALT_ININTERPRO; IPR000276; GPCR_Rhodpsn.pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and gene expression peptide receptor in rat tissues."; peptides 19:15-20(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.; "Molecular analysis of rat pituitary and hypothalamic grosscretagogue receptors.";
                                                                                                                                                                             G-protein
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stomach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20067959; PubMed=10604470;
KOjima M., Hosoda H., Date Y., Nakazato M., Matsuo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokote R., S
Takahara J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Wistar; TISSUE-Pituitary; MEDLINE-98100386; PubMed-9437732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pituitary; MEDLINE-97246555; PubMed-9092793;
                                                       DOMAIN
                                                                     TRANSMEM
                                                                                                            DOMAIN
                                                                                                                          TRANSMEM
                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                        EMBL; U94321; AAC53156.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:656-660(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Ghrelin_is a growth-hormone-releasing acylated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-240 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                               hormone releasing peptides (GHRP) (e.g. Met-enkephalin and as well as non-peptide, low molecular weight secretagogues L-692,429, MK-0677, adenosine) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Receptor for ghrelin,
                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through meen the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content by non-profit institutions as long as its content by find this statement is not removed. Usage by any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinol. 11:415-423(1997).
                                                                                                                                                                          coupled
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67
73
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                                                                                                                                                                                                                                                        BAA21777.1; ALT_INIT
                                                                                                                                                                             receptor;
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Rodentia;
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EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                                Transmembrane; Glycoprotein. EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
                                                                                                                       CYTOPLASMIC (P
2 (POTENTIAL).
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohye H., Niimi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor).
                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GHS-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
: Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GH-releasing
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MRL outstation ~
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                                                                                                                                                                                                                           REDLINE-YORKSHIP: TISSUE-Pituitary:

RA MEDLINE-96337998; PubMed-8688086;

RA HOWARD A.D., Feighner S.D., Cully D.F., Arena J.P.,

RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,

RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,

RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,

RA Achert K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,

RA McKee K.K., Pong S.-S., Chaung L.-Y., Elbrecht A., Dashkevicz M.,

RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,

RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,

RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,

RA Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,

RA Patchett A.A., Smith R.G., van der Ploeg L.H.T.;

RT Finctions in pituitary and hypothalamus that functions in growth

Normone release.";

RT FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.

CC -: FUNCTION: Receptor for ghrelin, coupled to G-alpha-12 proteins.

CC -: FUNCTION: Receptor for ghrelin, coupled to G-alpha-13 proteins.

CC -: FUNCTION: Receptor for ghrelin, coupled to G-alpha-13 proteins.

CC -: FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.

CC -: SUBCELLULAR LOCATION: Integral membrane protein.

CC -: SUBCELLULAR LOCATION: Integral membrane protein.

CC -: SUBCELLULAR LOCATION: Integral membrane protein.

CC -: SUBCELLULAR LOCATION: SIGNOWN HERE) AND 1B; ARE

CC -: SUBCELLULAR LOCATION: SIGNOWN HERE) AND 1B; ARE

CC -: SUBCELLULAR LOCATION: SIGNOWN HERE) AND 1B; ARE

CC -: SUBCELLULAR LOCATION: SIGNOWN HERE) AND 1B; ARE

CC -: SUBCELLULAR LOCATION: SIGNOWN HERE) AND 1B; ARE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95254; Q95255;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHSR_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
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                                                                                                                                                       SECRETAGOGUES.
TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSVYYVPIEVVGVIGNVLVCLVILQHQAMKTPTNYYLESLAVSDLLVLLLGMPLEVYEMW
                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIVWGFSVLFSLPNTSIHGIKFHYFPNGS-----LVPGSATCTVIKPMWIYNF
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                                                                              Swiss Institute
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364
197
13
26
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TO FAMILY
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CYTOPLASMIC (POTENTIA
BY SIMILARITY
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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                                                                      Bioinformatics
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No. 4
     removed.
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                                                                                                                                                                                         HYPOTHALAMUS
                                                                                                                                                             G-PROTEIN COUPLED RECEPTORS
                      There are no rest
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.2e-13;
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Sus.
                                               restrictions
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     for
                                                                              outstation
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  commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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Best Local
                                                                                                                                                                                                                                                                                       Matches
                                                                                 093603;
30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                     VARSPLIC
SEQUENCE
 SEQUENCE FROM N.A. TISSUE-Pituitary;
                                                                       Thyrotropin-releasing
                                         Archosauria; Aves;
                                                 Eukaryota; Metazoa;
                                                                  receptor)
                         NCBI_TaxID=9031;
                                                                                                                 TRFR_CHICK
                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U60178; AAC48630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U60180;
                                                                                                                                                          217
                                                                                                                                                                       213 IIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                                                                                                                                        165
                                                                                                                                                                                                                       105
                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                            45 VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                   GIVWGFSVLFSLPNTSIHGIKFHYFPNGS------LVPGSATCTVIKPMWIYNF
                                                                                                                                                                                                                             VTATCVALFVVGIAGNILTMLVVSRFREMRTTTNLYLSSMAFSDLLIFLC-MPLDLFRLW
                                                                                                                                                        -----SSVFFFLPVFCLTVLYSLIGRKL 239
                                                                                                                                                                                      LVIWAVAFCSAGPIFVLVGVE---HDNGTDPRDTNECRATEFAVRSGLLTVM--VWV---
                                                        gallus (Chicken).
                                                                                                                                                                                                                                                                                       66;
                                                                    (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
-releasing hormone receptor (TRH-R)
                                                                                                                                                                                                                                                                                                                     290
366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing
                                                                                                                                                                                                                                                                                     Conservative
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118
140
163
1184
212
212
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236
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286
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327
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                                                                                                                 STANDARD;
                                         Neognathae;
                                                                                                                                                                                                                                                                                                                     366
41194
                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
Veognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                 Pred. No. 4.207; Mismatches
                                                                                                                                                                                                                                                                                            Score 274;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                           N-LINKED (GICNAC. . .) (POTENTIAL).
N-LINKED (GICNAC. . .) (POTENTIAL).
AVVYFAPILCWLPEHVGRYLFSKS -> GGSQCAL
PLHSSCLFSSP (IN ISOFORM 1B).
MISSING (IN ISOFORM 1B).
                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
7 (POTENTTAI)
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.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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                                                                                                                                                                                                                                                                                     69;
                                                                       (Thyroliberin
                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                           -> GGSQCALELSLPG
                                       Phasianinae;
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Created)
Last sequence
Last annotation

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update)

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RESULT 11
GHSR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
GHSR_MOUSE STAN
Q99P50; Q91Z82;
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROUDUZ, GPCRRHODOPSN.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone receptor.";
Endocrinology 139:3390-3398(1998).
-!- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                            TVV----SCGYKVSRSYYSPIYMMDFGIFYVLPMVLATVLYGLIA
                                                                                                                                                                                                          SITAFTIERYIAICHPIKAQFLCTFSRAKKIIIFVWSFASVYCMLWFFLLDLNIAVYKDT
                                                                                                                                                                                                                                SITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNG
                                                                                                                                                                                                                                                                                                      TNYYLFSLAVSDLLVLL-LGMP---LEVYEMWRNYPFLFGPVGCYFKTALFETVCFASIL 132
                                                                                                                                                                                                                                                                           TNCYLVSLAVADLMYLVAAGLPNITESLYKSW-----VYGYVGCLCITYLQYLGINASSF
                                                                                                                                                                                                                                                                                                                                           QNHTGLLLSSQEFVT-----AEYQVVTILLVLLICGLGIVGNIMVVLVVLRTKHMRTP
                                                                                                                                                                                                                                                                                                                                                                         QKH----LNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTP
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                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 270.5; DB Pred. No. 8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..)
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CYTOPLASMIC (
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4 (POTENTIAL
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                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gershengorn M.C., Illing N.; of the chicken thyrotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291D9BD2718723CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                              257
                                                              ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                        23;
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(GHS-R) (GH-releasing

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Best Local
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                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY056474; AAL13336.1; -.
EMBL; AF332997; AAG61141.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peng X., Frohman L.A., Kinem Submitted (JAN-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                 G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-129S3/SvImJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA rapid amplification of cDNA ends (RACE).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orowin normone secretagogue receptor type 1 (GHS-R) (Ghipeptide receptor) (GHRP) (Ghrelin receptor) (Fragment). GHSR.
                                                                                                                                                              NON_TER
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kacsoh B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
 104
                          105
                                                 45
                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-as well as non-peptide, low molecular weight secretagogues (e.g. L-992,429, MK-0677, adenosine) (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
QYRPWNFGDLLCKLFQFVSESCTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVI
                      RNYPFLEGPVGCYFKTALFETVCEASILSITTVSVERYVAILHPFRAKLQSTRRRALRIL 164
                                                             VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                              VTATCVALFVVGISSNLLTMLVVSRFRELRTTTNLYLSSMAFSDLLIFLC-MPLDLVRLW 103
                                                                                                                                                                                                                                                                                                                                                                                                                 PF00001; 7tm_1;
                                                                                                 65;
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                          PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
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126 148
149 160
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28743 MW;
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                                                                                                                                                                                                                                                                                                                                                                receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                                             21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kineman
                                                                                                 47;
                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
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                                                                                                             Score
Pred.
                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                 BY SIMILA
                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.D.;
                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                 D6FA21EAB0E30791
                                                                                                 Mismatches
                                                                                                                                                                                                             SIMILARITY
                                                                                                           268;
45. 8.
                                                                                                                                                                     (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
                                                                                                                       DB 1;
                                                                                                             2e-13;
                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                70;
                                                                                                                                                 CRC64;
                                                                                                                      Length 257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
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RESULT 12
TRFR_MOUSE
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 δõ
                            G-protein
DOMAIN
                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P21761;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                   EMBL; M59811; AAA40480.1; -.
EMBL; M94384; AAA40437.1; -.
EMBL; L48936; AAA81559.1; -.
PIR; A39251; A39251.
                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                          Jones K.E., Brubaker J.H., Chin W.W.; "An alternative splice variant of the mouse TRH receptor mRNA is the major form expressed in the mouse pituitary gland."; J. Mol. Endocrinol. 16:197-204(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straub R.E., Frech G.C., Joho R.H., Gershengorn M. "Expression cloning of a cDNA encoding the mouse p thyrotropin-releasing hormone receptor.";
Proc. Natl. Acad. Sci. U.S.A. 87:9514-9518(1990).
                                                                                                                       MGD;
                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Narayanan C.S., Fujimoto J., Geras-Raaka E., Geraglation by thyrotropin-releasing hormone ("Regulation in rat pituitary GH3 cells."; mRNA degradation in rat pituitary GH3 cells."; J. Biol. Chem. 267:17296-17303(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pituitary;
MEDLINE=91088548; PubMed=2175902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRHR.
 DOMAIN
                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97013702; PubMed=9156522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92381047; PubMed=1324930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRFR_MOUSE
                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 332-393 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE. RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
            PF00001; 7tm_1; 1.

TE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

TE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Tein coupled receptor; Transmembrane; Glycoprotein.

Stein coupled receptor; STRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                       MGI:98824; Trhr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVIWAVAFCSAGPIFVLVGVEHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIVWGFSVLFSLPNTSIHGIKFHYFPNGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVFFFLPVFCLTVLYSLIGRKL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
 529
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
1 receptor;
28
51
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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 (POTENTIAL)
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-93371401; PubMed=8395824;
Matre V., Karlsen H.E., Wright M.S., Lundo
Matre V., Karlsen H.E., Gautvik K.

""" a functional human
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                TRHR.
Homo sapiens (Human).
'--rvota; Metazoa; Chordata;
'--ria; Primates;
expression gene.";
      Kakegawa T., Mori M.;

"Pituitary adenomas of patients with acromegaly express thyrotropin-
releasing hormone receptor messenger RNA: cloning and functional
expression of the human thyrotropin-releasing hormone receptor
                                                              TISSUE=Pituitary; MEDLINE=93384596;
                                                                                                           Biochem.
                                                                                                                                                                                                                                                               Thyrotropin-releasing
                                                                                                                                                                                                                                                                         01-FEB-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                             P34981;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                    TRFR_HUMAN
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                                                   Yamada M., Monden
                                                                                                                     hormone receptor.
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                                                                                                         Biophys.
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                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                   PubMed=8396925;
T., Satoh T., Satoh N.,
                                                                                                           Res.
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Last annotation update)
hormone receptor (TRH-R
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                                                                                                         Commun.
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Pred. No.
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N-LINKED (GLCNAC. . .)
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4 (POTENTIAL)
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5 (POTENTIAL).
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3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                          Lundell I., Fjeldheim
ik K.M.;
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                                                   Murakami M.,
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                                                                                                                                                                                                                                                            (Thyroliberin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 393;
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                                                    Iriuchijima
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EMBL; D16845; BAA04120.1; EMBL; X75071; CAA55965.1; -
EMBL; X75071; CAA5979-1; -
EMBL; X75283; AAB32222.1; -
EMBL; S75281; AAB32222.1; -
EMBL; S75281; AAB32222.1; -
EMBL; D85376; BAA12796.1; -
EMBL; D85376; BAA12796.1; -
EMBL; D85375; BAA12796.1; -
EMBL; EMBL; EMBL;
                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human thyrotropin releasing hormone receptor.";
J. Neurochem. 72:40-50(1999).
-i- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.
-ERECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                  G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matre V., Hovring P.I., Velickovic Z., Murray-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
MEDLINE=99101143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kohga H., Kato Y., Mori M.;
"Genomic organization and promoter function releasing hormone receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Duthie S.M., Tayl
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                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watre V., Hovring P.I., Orstavik S., Frengen E., Ria Velickovic Z., Murray-Mcintosh R.P., Gautvik K.M.; Velickovic Z., Murray-Mcintosh R.P., Gautvik K.M.; "Structural and functional organization of the gene human thyrotropin-releasing hormone receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iwasaki T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JN0708;
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S40682; S40682.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:12299;
                                                                                                                                                                                      PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_1; 1.
PS502626; G_PROTEIN_RECEP_F1_1; 1.
PS502626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF 1-263 FROM N.A.
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i M.;
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                         EXTRACELLULAR
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                      CYTOPLASMIC
2 (POTENTIA)
     EXTRACELLULAR
                                                                                                                                      (POTENTIAL)
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046639;
16-0CT-2001
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DOMAIN
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                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                           gene.";
J. Vet. Med. Sci. 60:123-127(1998).
-i- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING
                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Co
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                     BOVIN
                      EMBL; D83964;
                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                    MEDLINE-98151337; PubMed-9492373;
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                  Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                              "Molecular cloning of bovine thyrotropin-releasing
                                                                                                                                                                                                                                                    STRAIN-Holstein;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      receptor).
                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
16-OCT-2001
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                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                      FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE. RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQVTSFLFYLLPMTVISVLYYLMA
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Eutheria; Cetartiodactyla: Ruminantia: Processioni;
          IPR000276;
                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
-releasing hormone receptor (TRH-R) (Thyroliberin
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Pred.
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N-LINKED (GLCNAC...) (
N-SK (IN DBSNP:5774).
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No. 5.
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                                                  (See http://www.isb-sib.ch/announce/
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RESULT 15
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01-NOV-1997
01-NOV-1997
15-JUL-1998
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CARBOHYD
                                                                                                                      TISSUE=Pituitary;
MEDLINE=97200775; PubMed=9048604;
                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                          SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein
DOMAIN
 -!- SUBCELLULAR
-!- SIMILARITY:
                    ENDOCTIONOLOGY 138:1019-1028(1997).

-I- FUNCTION: RECEPTOR FOR THYROTROPIN-RELEASING HORMONE.

-RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                     Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                    Thyrotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; PROSITE; PS50262;
                                                                  "Thyrotropin expression in hypophyseal pars tuberalis-specific is 3,5,3'-triiodothyronine, thyrotropin-releasing hormone, and independent.";
                                                                                                    Bockmann J., Boeckers T.M., Deufel T., Kreutz M.R.;
                                                                                                                                                  SEQUENCE FROM N.A.
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Metazoa;
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7 (Rel. 35, I
8 (Rel. 36, I
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                                                                                                                                                                                                                                                                                                             STANDARD;
LOCATION: Integral membrane protein.
BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 receptor; 2
28
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G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                             Chordata; Craniata; Vertebra
Cetartiodactyla; Ruminantia;
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                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                    hormone receptor (TRH-R) (Thyroliberin
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                Winter C.,
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CYTOPLASMIC (F
6 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)

7 (POTENTIAL)
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N-LINKED (GLCNAC. ..)
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CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                        215
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                                                                                                                                                                                                                                                                                                             398
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                                                                                                              Wittkowski W.,
                                                                                                                                                                                              Vertebrata; Euteleostomi;
minantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                             A
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                                                                                                                Winterhoff
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Best Local Similarity
Matches 66; Conserv
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CARBOHYD
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DOMAIN
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X95285; CAA64606.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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198 V------FYVVPMILATVLYGFIA 215
                                                                                                                                                                                                                                                   100 VYEMWRNYPELFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPERAKLQSTRRR 159
                                                         214 IQVTSFLFYLLPMTVISVLYYLMA 237
                                                                                                                     142
                                                                                                                                                       160 ALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATC----TVIKPMWIYNFI 213
                                                                                                                                                                                                                                                                                                                                                                87 IYGSW-----VYGYVGCLCITYLQYLGINASSCSITAFTIERYIAICHPIKAQFLCTFSR 141
                                                                                                                                                                                                                                                                                                                                         27
                                                                                                       AKKIIIFVWAFTSIYCMLWFFLLDLNISTYKDAIVV----SCGYKISRNYYSPIYLMDFG 197
                                                                                                                                                                                                                                                                                                                             VTILLVLIICGLGIVGNIMVVLVVMRTKHMRTPTNCYLVSLAVADLMVLVAAGLPNITDS 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).;
375A311D3DD2A61A CRC64;
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7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Earch completed: January 17, 2003, 05:04:48

5.1.3

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 20
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1263
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Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapext 0.5
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75.166 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Query

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255	255	255	255	255	255	255	255	255	255	255	256.5	262.5	262.5	262.5	262.5	262.5	262.5	418	Score
20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.2	20.3	20.8	20.8	20.8	20.8	20.8	20.8	33.1	Match Length
444	438	409	401	398	398	398	398	392	391	390	415	259	259	259	259	259	222	419	
10	10	10	10	12	10	10	10	10	10	10	10	10	9	9	9	9	10	10	DB
us-09-761-962-28	US-09-761-962-17	US-09-761-962-27	US-09-761-962-20	US-10-039-645-83	US-09-966-871-83	US-09-761-962-29	US-09-214-904-2	US-09-761-962-19	US-09-761-962-26	US-09-761-962-25	US-09-823-114-20	US-09-796-338A-23	US-10-077-698-3	US-10-012-140-29	US-10-012-140-27	US-10-080-960-25	US-09-911-005-4	US-09-804-551B-26	ID
Sequence 28, Appl	Sequence 17, Appl	Sequence 27, Appl	Sequence 20, Appl	Sequence 83, Appl	Sequence 83, Appl	Sequence 29, Appl	2,	Sequence 19, Appl	26,	Sequence 25, Appl	20,	e 23	Sequence 3, Appli	Sequence 29, Appl	Sequence 27, Appl	Sequence 25, Appl	Sequence 4, Appli	Sequence 26, Appl	Description

RESULT 2

254.5 20.2 405 12 US-10-039-645-84 253.5 20.1 400 12 US-10-039-645-85 253.5 20.1 400 12 US-10-039-645-87 253.5 20.0 383 10 US-09-966-871-87 253.2 20.0 383 12 US-10-039-645-87 251.5 19.9 400 12 US-10-039-645-86 251.5 19.9 400 12 US-10-039-645-86 241.5 19.5 400 10 US-09-863-871-87 246.5 19.5 400 12 US-10-039-645-78 244.5 19.5 400 12 US-10-039-645-78 244.5 19.2 367 10 US-09-823-114-23 242.5 19.2 387 10 US-09-9823-114-23 242.5 19.2 387 10 US-09-93-844-4 242.5 19.2 388 10 US-09-966-871-11 242.5 19.2 398 11 US-09-966-871-81 242.5 19.2 398 12 US-10-039-645-1 242.5 19.2 398 12 US-10-039-645-81 242.5 19.2 398 12 US-10-039-645-81 242.5 19.2 359 10 US-09-966-871-81 242.5 19.2 359 10 US-09-966-871-79 243.5 19.0 398 12 US-10-039-645-91 240.5 19.0 398 10 US-09-966-871-79 240.5 19.0 398 10 US-09-966-871-79 240.5 19.0 398 10 US-09-966-871-79 241.5 19.2 359 10 US-09-966-871-79 242.5 19.2 359 10 US-09-966-871-79 243.5 19.0 398 10 US-09-966-871-79 243.5 19.0 398 10 US-09-966-871-79 243.5 19.0 398 10 US-09-966-871-79 244.5 19.0 398 10 US-09-966-871-79 245.5 19.0 398 10 US-09-966-871-79 246.5 19.0 398 10 US-09-966-871-79 247.5 19.0 398 10 US-09-966-871-79 248.5 19.0 398 10 US-09-966-871-79 249.5 19.0 398 10 US-09-966-871-79 240.5 19.0 398 10 US-09-966-871-79 241.5 19.0 398 10 US-09-966-871-79 242.5 19.0 398 10 US-09-966-871-79 243.5 19.6 450 9 US-09-867-915-3	45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21
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	453	460	370	359	359	398	398	359	359	398	398	398	382	367	506	400	400	369	400	400	383	383	400	400	405
US-10-039-645-84 US-09-966-871-85 US-10-039-645-87 US-10-039-645-87 US-10-039-645-87 US-10-039-645-86 US-10-039-645-87 US-10-039-645-78 US-10-039-645-78 US-10-039-645-78 US-10-039-645-78 US-10-039-645-78 US-09-966-871-11 US-10-039-645-71 US-10-039-645-71 US-10-039-645-79 US-09-966-871-79 US-09-867-569-9 US-09-867-569-9 US-09-867-569-9 US-09-867-569-9 US-09-970-966-209	9	9	10	10	9	12	10	12	10	12	10	10	10	10	10	12	10	10	12	10	12	10	12	10	12
	US-09-970-966-209	US-10-166-101-4	US-09-823-114-19	US-09-867-569-9	US-09-867-915-3	US-10-039-645-79	US-09-966-871-79	US-10-039-645-81	-09	-10	US-09-966-871-1	US-09-823-114-16	US-09-993-844-4	US-09-823-114-23	-09-804-551B-	US-10-039-645-78	US-09-966-871-78	-09-823-114	-10-039-645	US-09-966-871-86	US-10-039-645-87	US-09-966-871-87	US-10-039-645-85	-09-966-871-	US-10-039-645-84

#### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09804551B
Patent No. US20020056151A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Receptors for peptides from insects
FILE REFERENCE: Le A 34 394
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 26
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/804,551B CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 100 13 618.4 PRIOR FILING DATE: 2000-03-18 NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                                       LENGTH: 419
TYPE: PRT
ORGANISM: Drosophila melanogaster
   183
                                                                131
                                                                                                 153
                              213 IIQVTSFLEYLLPMTVISVLYYLMALRV 240
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                                                                                                                                             93 LLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAK 152
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                                                                                                                              --QLSTFIFFLAPMSIILVLYLLIGVHL 208
                                                               AMSKLSRAIRIIVLVWIMAIVTAIPQAAQFGIE-HY-----SGVEQCGIVRVIVKHSF 182
                                                                                             LQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNF 212
                                                                                                                                                                                                                                                              85;
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                                                                                                                                                                                                                                                                               33.1%; Score 418; DB 10; 40.9%; Pred. No. 1e-32;
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; OTHER INFORMATION: Consensus amino acid sequence US-10-080-960-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/10080960 Publication No. US20020197695A1 GENERAL INFORMATION:
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SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 222
TYPE: PRT
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APPLICANT: GLUCKSMANN, MARÍA ALEXANDRA
TITLE OF INVENTION: 65494, A NOVEL HUMAN G-PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR FAMILY MEMBER AND USES THEREF
FILE REFERENCE: 10448-075001
                                                                                                          SEQ ID NO 25
LENGTH: 259
                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/241,992
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 67; Conserv
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                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/242,040
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Meyers, Rachel TITLE OF INVENTION: 80090, 52874,52880,63497, TITLE OF INVENTION: METHODS AND COMPOSITIONS FILE REFERENCE: 38155-20044,00 CURRENT APPLICATION NUMBER: US/10/080,960 CURRENT FILING DATE: 2001-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Millennium Pharmaceuticals, APPLICANT: Glucksmann, Maria
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CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 60/220,042
PRIOR FILING DATE: 2000-07-21
                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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OF HUMAN PROTEINS AND USES THEREOF
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Best Local Similarity
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
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Best Local Similarity
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 18560, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 259
175
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                                   224 LPMTVISVLY
                                                                          116 LLLSLPPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTWLRSYVL-LSTLVGFL 174
                                                                                                           172 VLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKP------MWIYNFIIQVTSFLFYL 223
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LPLLVILVCY 184
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                                                                                                                                                                                                                                                                                                                                   Score 262.5; DB 9
Pred. No. 4.7e-18;
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Pred. No. 4.7e-18;
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CURRENT APPLICATION NUMBER: US/10/077,698
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/261,599
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/27,761
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR APPLICATION NUMBER: 09/223,538
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 259
LENGTH: 259
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10077698 Publication No. US20030008350A1 GENERAL INFORMATION:
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 36550, 28472, 5495,
TITLE OF INVENTION: 14354 METHODS AND
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/246 768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246 772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14273 Receptor, A No. US20030008350Alel G-Protein Coupled Receptor FILE REFERENCE: 5800-4B, 035800/177086
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CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
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ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 SALCKLYTALDYVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVWVLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVY-----EMWRNYPFLFG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNLLVILVILRTKKLRTPTNIFILNLAVADLLFLLTLPPWALYYLVGGSEDWP-----FG 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.8%; Score 262.5; DB 9 35.3%; Pred. No. 4.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOSITIONS OF HUMAN PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
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US-10-077-698-3
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US-09-796-338A-23
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                                                                                                                                                                                                                                                                                                                                                                                          US-09-796-338A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 259
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09796338A
Patent No. US20020061522A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEF
FILE REFERENCE: 10448-020001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: consensus sequence
  175
                                                                           116
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                                    224
                                                                                                                                                                                         113 PVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR-RRALRILGIVWGFS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 LPMTVISVLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 PVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR-RRALRILGIVWGFS 171
                                                                                                              172 VLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKP-----MWIYNFIIQVTSFLFYL 223
                                                                                                                                                                                                                                                    59 GNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVY-----EMWRNYPFLFG 112
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                                                                                                                                                    56 SALCKLYTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVMVLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 SALCKLVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRRAKVVILLVMVLA 115
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                                LPMTVISVLY
                                                                         LLLSLPPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTWLRSYVL-LSTLVGFL 174
                                                                                                                                                                                                                                GNLLVILVILRTKKLRTPTNIFILNLAVADLLFLLTLPPWALYYLVGGSEDWP-----FG 55
LPLLVILVCY
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                                                                                                                                                                                                                                                                                                             Conservative
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Transmembrane Segment Rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%;
                                                                                                                                                                                                                                                                                                         20.8%; Score 262.5; DB 1 35.3%; Pred. No. 4.7e-18; Live 38; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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Pred. No. 4.7e-1
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                                                                                                                                                                                                                                                                                                                                                  DB 10;
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                                                                                                                                                                                                                                                                                                             64;
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US-09-823-114-20; Sequence 20, Application US/09823114

RESULT

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                170
                                                                                                                                                         137
248 LIITVCYGLMILRL 261
                                    227 TVISVLYYLMALRV 240
                                                                            196
                                                                                                                                                                                     110 LFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWG 169
                                                                                                                                                                                                                                                   30
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                                                                                                                                                                                                                             79 IVCVVGLEGNELVMYVIVRYTKMKTATNIYIENLALADALATST-LPEQSVNYLMGTWP- 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EVANS, CHRISTOPHER J. KEITH, DUANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                              SWV----
                                                                        LSSAIGLPVMFMATTKYR
                                                                                                            FSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVI--KPMWIYNFIIQVTSFLF-YLLPM 226
                                                                                                                                                  -FGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDFRTPRNAKIINVCNWI 195
                                                                                                                                                                                                                                                                                                                                              SWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF------FLPVSVVYV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: group(9, 12, 33, 40, 48)
OTHER INFORMATION: /note= "extracellular Asn residues
that are consensus sites for N-linked glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/OCCKET NUMBER: 22000-20526.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/823,114
FILING DATE: 29-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/148,351
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 256.5;
Pred. No. 3e
                                                                        QGSIDCTLTFSHPTWYWENLVKICVFIFAFIMPV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20:
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RESULT

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US-09-761-962-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
                                                                                                                                                                                                                                                                SEQ ID NO 26
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization of Multiple Splice
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application U. Patent No. US20020077285A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0 SEQ ID NO 25
                                                                                                                            Best Local Similarity Matches 70; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
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TYPE: PRT
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77 TNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
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Pred. No. 3.9e-17;
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Pred. No. 3.9e-17;
2; Mismatches 84
                                                                                                                            Mismatches
                                                                                 --VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTP 76
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 392
Type: """
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Patent No. US20010047519A1
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: Opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/743,872
PRIOR FILING DATE: 2001-03-13
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atent No. US20020077285A1
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                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICATION DATA:
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                                                                                                                                                                      TRANSGENIC ANIMAL IN WHICH THE EXPRESSION OF OPIATE RECEPTORS IS MODIFIED 6
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                                     US/09/214,904
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Pred. No. 3.9e-17;
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US-09-761-962-29
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APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REFERENCE: 830002-2000.1
CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
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LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/743,872 PRIOR FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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LENGTH: 398 amino acids
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QGSIDCTLTESHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL
                                                                                  TVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLV 195
                                                                                                                   TNIYIFNLALADALATST-LPFQSVNYLMGTWP--FGNILCKIVISIDYYNMFTSIFTLC 159
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                                                                                                                                                   TNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
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                                                                                                                                                                                                                                                                     Score 255; DB 1
Pred. No. 4e-17;
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Pred. No. 4
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В

212 QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL 259

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-966-871-83
Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83, Application US/10039645 Patent No. US20020147170A1
                                                                                                                                                                                                                                          APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: Constitutively Active, Hypersensitive,
TITLE OF INVENTION: and No. US20020147170Alfunctional Receptors as No. US20020147170
FILE REFERENCE: 00398/510002
CURRENT APPLICATION NUMBER: US/10/039,645
CURRENT FILING DATE: 2001-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOPIN, Alan S.

APPLICANT: KOPIN, Alan S.

TITLE OF INVENTION: Assays for Identifying Receptors Having TITLE OF INVENTION: Alterations in Signaling FILE REFERENCE: 00398/512002

CURRENT APPLICATION NUMBER: US/09/966,871

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US 60/236,302

PRIOR APPLICATION NUMBER: US 60/288,644

PRIOR FILING DATE: 2001-09-28

PRIOR FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/243,550
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 PGSATCTVI--KPMWIYNFIIQVTSFLF-YLLPMTVISVLYYLMALRV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNIYIFNLALADALATST-LPFQSVNYLMGTWP--FGNILCKIVISIDYYNMFTSIFTLC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYR------
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    Conservative
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                    20.2%; Score 255; DB 12; 30.7%; Pred. No. 4e-17;
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Mismatches
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                                     Length 398;
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QGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITVCYGLMILRL 259
                                                                          TMSVDRYIAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYR---
                                                                                                                                                  TNIYIFNLALADALATST-LPEQSVNYLMGTWP--FGNILCKIVISIDYYNMFTSIFTLC 159
                                                                                                                                                                                      TNYYLFSLAVSDLLVLLLGMPLE-VYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
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                                      PGSATCTVI -- KPMWIYNFIIQVTSFLF-YLLPMTVISVLYYLMALRV 240
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Search completed: January 17, 2003, 05:09:27 Job time: 67 secs

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Result
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Maximum DB seq
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  528
488.4
354.2
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(without alignments)
5366.595 Million cell updates/sec
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Compugen Ltd.
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BM737726
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601448032
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BI224313	вJ499680	AK020259	BE266564	AK005368	вв656301	BI872266	BE746231	BB642318	BH160272	AZ548467	AZ551618	BE654347	CNS04SGJ	BF446062	BI600170	BI873140	BB642387	BI753905	BG714306	BM546496	AK004891	BC018330	BI463235	BM808823	BM808829	BI757121	BM925480	CNS020N1	CNEORGRA	BF323227	BM543497	BF603623	CNS01XJ2	CNS04GXP	AU244285	AU244292	CNS036WH	BQ721315
224313 6029	J499680 BJ499	.K020259 Mus m	66564	05368	56301	72266	46231	42318	60272	48467	51618	347	05164	46062	00170	73140	42387	53905	14306	46496	04891	18330	63235	08823	08829	57121	BM925480 AGENCOURT	09492	2 1 2 1	2322	43497	BF603623 269181 MA	71767	L29023(	244285 AU	44292 AU2442	570 Te	721

# ALIGNMENTS

TITLE JOURNAL COMMENT KEYWORDS SOURCE ORGANISM ACCESSION VERSION FEATURES REFERENCE DEFINITION POCUS AUTHORS source sequence. BM737726 BM737726.1 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 540)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Email: yongsung@mail.kribb.re.kr plate: 16 row: A column: 04 High quality sequence stop: 540. Location/Qualifiers Unpublished (2002) Contact: Kim YS BM737726 K-EST0000769 S1SNU5 Homo 21C Frontier Korean EST Project 2001 Kim, Y.S. Homo sapiens numan. GI:19059055 540 bp mRNA linear EST 01-MAR-2002 sapiens cDNA clone S1SNU5-16-A04 5', mRNA

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RESULT 2
AG046172/c
        DEFINITION
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Best Local
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                                                                                                 CTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGGCGCGCGGGGCCT 482
                                                                                                                                                                                                                                                                                                                                                                       CTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTA
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       Pan
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     troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Lymphoblast-like"
/cell_line="SNU-5"
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/tissue_type="Ascites"
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/clone_lib="S1SNU5"
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/db_xref="taxon:9606"
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99.8%;
   DNA,
 670 bp DNA clone: PTB-025E24.R,
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Pred. No. 1.7e-110;
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 genomic
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   survey
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                                                                                                                                                                                                             CAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGG
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                                                                                                                                                                                                                                                                                                 CTTCAAGACGGCCCTCTTTGAGACCGTGTGCCTTCGCCTCCATCCTCAGCATCACCATCACCT
                                                                                                                                                                                                                                                                                                                                                CCTGNAGGTCTATGAGATGTGGCGCAACTACCCTATCTTGTTCGGGCCCGTGGGCTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone tracking errors.
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Totoki,Y., Watanabe,H. and Sakaki,Y
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC end sequences of Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes
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AG046172.1
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R.Site 1
R.Site 2
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/clone_lib="PTB Chimpanzee
/c157 c 213 g 138 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="PTB-025E24.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
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Pred. No. 2.1e-101;
0; Mismatches 7;
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                                                   AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGAGCCTCGGCGCAGCCAC 120
                                   AAATACCTGAACAACACAGATGACTACCTAGCTTTGCTCTGCGGGCCTCGTCGCAGCCAC
                                                                                                       ATGGAAAAACATGAGAATGTTTCCTGGATGTACCAACAGGAACTGAAAGATCCTTTCAAG 168
                                                                                                                                                                             389;
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BE751626
BE751626.1 GI:10165618
EST.
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Flate: 44 row: O column: 6
Seq primer: ATTTAGGTGCACGTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cal
v0.980904.e. Vector identified by
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cow.
Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                             /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sa Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                          Score 354.2; DB 12; Pred. No. 9.7e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCCTGGAGGTC
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     481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BE871983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia; Eutheria: Primates: Catarrhini; Hominidae: 1 (bases 1 to 929)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE871983 929 bp mRNA linear EST 20-OCT-2000 01448032F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852151 5',
                                                                                                                                                                                                                                                                                         High quality sequence start: 11
High quality sequence stop: 602
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Plate: LLAM9573 row: p column:
                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                   Similarity
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                                                                                        186
     Conservative
                                                                                 Technologies. "
a 252 c 228 g
                                                                                                    /lab_host="DH10B (phage-resistant)"
/note="Organ: colon: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3852151"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                              . 929
                   43.2%;
Score 315; DB Pred. No. 1.1e 0; Mismatches
     0,
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                   DB 12;
L.1e-61;
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1 ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG

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SOURCE
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BB587450
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                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCCGGGCCTCAGGAATCTCCGGAATTCTCTGGGGCTACTCCGAGCACTTCTCCCTG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCCTGGTGTGCCTGGTGATCCTGCAGCCACCAGGCTATGAAGACGCCCACCAA-TACTA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGCGCTATGAAGACGCCCCACCAACTACTA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTTGTGGTGGGGGGCAATTGGCAA 179
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                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                            Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Ko,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasa,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., D., Tayawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibatta,Y., Hayatsu,N
,M., Konno,H., Okazaki,Y., Muramat:
                                                                                                                                                                                                                                                Unpublished (2001)
On Nov 30, 2000 this sequence version replaced gi:11483994
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 624)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus cDNA clone 993
BB587450
BB587450.2 GI:16449720
                                                                                                        Fax: 81-45-503-9216
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  Shibata, Y., Hayatsu, N., Okazaki, Y., Muramatsu
nyatsu,N., Sugahara,Y., Shibata
Muramatsu,M. and Hayashizaki,Y
                                                                                                                                                                                                                                RIKEN Genomic
                    Shibata, K.,
                                                                                                                                                    230-0045,
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151 AAGTACTTGAACAGCACAGAGGAGTACTTGGCCTACCCTGTGTGGACCCAAGCGCAGTGA

210

AAACACCTGAACAGCACCGAGGAGTATCTGGCCT-TCCTCTGCGGACCTCGGCGCAGCCA 119

CTATCCCTTCCAGTGTCTGTGGTCTATCCCCTGATCTTCGTGGTGGGGGTGATAGGCAA CTTCTTCCTCCCCGTGTCTGTGGGTGTATGTGCCAATTTTTTGTGGTGGGGGGCATTGGCAA 179 DЪ Qy

106

ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG 60

Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system -- 384 - format
                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
                                                                                                                                                                                     /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="vagina"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="9930001G13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length
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  38.4%;
77.1%;
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Score 280; DB 10; Pred. No. 9.4e-54;
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BE751310.1 GI:10165239
EST.
Cow.
Bos taurus
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Tel: 40
Fax: 40
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                  and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca.
v0.980904.e. Vector identified by
and -minmatch 12 options.
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Genome Res. 11 (4),
21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
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                                                                                                                                                                       Plate: 43
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te: 43 row: O column: 6
primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                        402 762 4366
402 762 4390
                                                    /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
          /note="Vector: pCMV SPORT6; Site_1: NotI; Si
Library made from pooled tissue from testis,
semitendonosus muscle, longissimus muscle, p
                                                                                                                                            Location/Qualifiers
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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and endometrium
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                                                      /dev_stage="adult, 16
/lab_host="DH10B"
                                                                                             /sex="male"
                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution MGC clone distri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ721315 993 bp mRNA AGENCOURT_8296894 Lupski_sympathetic_trunk IMAGE:6194542 5', mRNA sequence.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLAM13599 row: o column:
/note="Vector: pCMV-SPORT6 (Life Technologies); Si NotI; Site_2: SalI; cDNA made by Oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6194542"
                                                                                                                                                                                                                             /tissue_type="sympathetic
/dev_stage="adult, 16 yr"
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Lupski_sympathetic_trunk"
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Pred. No. 9.5
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                                                                                                                                              GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                  Roest-Crollius,H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided
                                 Tetraodon nigroviridis
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AL230570
AL230570.1 GI:7889565
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126 c 308 g 198 t 1 others
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                      AU244292 624 bp mRNA linear EST 15-JAN-2002 AU244292 Medaka eye cDNA library (SNK01) Oryzias latipes cDNA clone NGY47.02e similar to pir|T15816|hypothetical protein C48C5.1 - Caenorhabditis elegans, mRNA sequence.
AU244292
AU244292.1
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This sequence is a single read and was generated scale clone-end sequencing project of the Tetraod genome. For more information, please take a look http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission
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                                                              CTGCATGGCATCTTCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biological Sciences Graduate School of Science, Nagoya University Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan Tel: 81-52-789-2973
Fax: 81-52-789-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M. Medaka EST analysis Unpublished (2001)
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clone was isolated from Meda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryzias latipes"
/strain="wild type"
/db_xref="taxon:8090"
/clone="NGY47.02e"
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/tissue_type="eye"
/dev_stage="adult"
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clk 109K06 of library G from Tetraodon nigroviridis, genomic survey sequence. ALZ90Z30
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos:
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele:
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beioniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences Graduate School of Science, Nagoya University Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan Tel: 81-52-789-2973
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Sanaka, E., Hori, H., Naruse, K., Mitani, H. and Tanaka, M. Medaka EST analysis
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This clone was isolated from Medaka
Location/Qualifiers
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Contact: Emi Sanaka
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NGY47.01f, mRNA sequence.
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/strain="wild type"
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/clone="NGY47.01f"
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/tissue_type="eye"
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                                    GGCCCTCAGGATCCTCGGCATCGTCTGGGGCCTTCTCCGTGCTCTTCTCCCTGCCCAACAC
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GGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCCAAACTGCAGAGCACCCGGCGCCG
                                                                                                                                                CAACTTCCTGTTCGAGGCGTGCAGCTACGCCACCATTGTGAACATAGCCACGCTTAGCTT
                                                                                                                                                                                                                         CTACAGCGCCATCTGGTTCCCCTTCACCTCGGCGTCCGGCAACGTCTCCTGTAAGAWCTA
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fizameau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Human gene number estimate provided by genome wide analysis using
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ACKTCTCCTGTAAGATCTACAACTTCCTGTTCGAG-GCGTGCAGTACGCCACCATTGTGA
                                                                                                                      TTGGAATGCCCCTGGAGGTCTA---TGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGC
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1 (bases 1 to 817)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., F Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, Saurin, W. and Weissenbach, J.
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Tetraodon nigroviridis
Tetraodon nigroviridis
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Direct Submission
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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202F23 of
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1 237 c 258 g 159 t 5 others
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/db_xref="taxon:99883"
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                                                                                                                                                Local Similarity
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                    CCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCACCAACTACTACCTCTTCAGCCT
                                                     CGTCACAGCCACCTGCGTGGCGCTCTTCGTGGTGGGCATCGCGGGCAACCTGCTCACCAT 126
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Mammalia; E
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Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T. Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C. Certea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF603623
BF603623.1 GI:11701421
EST
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269181 MARC 3BOV Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
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1 (bases 1 to 50
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                                                                                                                               Conservative
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                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Eutheria; Cetartiodactyla; Ruminantia; Pec
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Ruminantia; Pecora;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: e column: 24
High quality sequence stop: 635...
Location/Qualifiers
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1 (bases 1 to 1027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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BM543497
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    153
                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726591"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
                  /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
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Query Match Best Local Similarity

13.4%; 51.9%;

Score 97.6; DB Pred. No. 5.9e-1

13;

1027;

Conservative

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Mismatches

Length Indels

9;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BF323227
BF323227.1
EST.
house mouse.
MGI:1455149
Seq primer:
                                                                 (CGAP/BTGAP), Tumor Gene Index (1998)
Other_ESTS: maa38a07.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 448)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
"-------14a. Futheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF323227

448 bp mrNA linear EST 21-NOV-2000 maa38a07.yl NCI_CGAP_Brn63 Mus musculus cDNA clone IMAGE:3813037 5' similar to SW:NTR2_RAT Q63384 NEUROTENSIN RECEPTOR TYPE 2 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:11272778
    -40RP
    from
  Gibco
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Search comp Job time :

completed: January 17, me : 2233 secs

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Best Local S
Matches 208
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ATGGGACAGAAGCACGA
                                                                            AGGATCCTCGGCATCGTCTGGGGCTTCTCCCGTGCTCTTCTCCCTGCCCAACACCAGCATC
                                                                                                                      TGCCTGGCCGTGTGCCAGCCGCTGCGCGCCCCCGCCTGCTCACCCGCGCACCCGC
                                                                                                                                                                                                               CTCTTTGAGACCGTGTGCCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGC
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                            CATGGCATCAAGTTCCA 560
                                                            CGCCTGCTGTCACTGGGTCTGGGTCGCCTCTCTGGGCCTTGCCCCTGCCCCATGGCGGTTATC
                                                                                                                                                   GTGCGCGAGCTGTGCGCCTACGCCACGGTGCTGAGCGTGGCCAGCCTGAGCGCAGAGCGC
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08; Conservative
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Location/Qualifiers
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
157 c 148 g 89 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3813037"
/clone_lib="NCI_CGAP_Brn63"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
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55.2%;
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Pred. No. 1.3e-11;
0; Mismatches 166;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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length: 2000000000
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     Published_Applications_NA: *
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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10 US-09-967-768A-296

9 US-09-970-966-208

10 US-09-825-294-208

10 US-09-829-631A-12

10 US-09-917-800A-1620
                                                        US-10-077-870-3
US-09-825-923-3
US-10-044-090-444
US-10-052-589-1
US-09-964-824A-249
US-09-940-240-15
US-09-954-531-995
                                                                                                                                                              US-10-077-870-1
US-09-825-923-1
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US-09-104-063-5
US-10-090-569-6
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Sequence 25, Appl
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Sequence 128, Appl
Sequence 12, Appli
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Sequence 3, Appli
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Perfect score: Sequence:

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66.4	67.2	67.2	68.4	68.4	68.4	69.6	70.4	70.4	70.4	70.6	73.4	73.4	73.6	73.6	73.8	73.8	74.4	74.4	74.8	74.8	74.8	75.2	75.2	75.2	75.2
9.1		9.2		9.4	9.4	9.5	9.7	9.7	9.7	9.7	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.3	10.3	10.3		•	10.3	10.3
1149	1272	1272	1609	1197	1197	823	1710	1296	1296	1773	720	720	1829	1829	1895	1670	2108	1914	2602	2081	2080	1882	1829	1829	1829
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US-09-993-844-10	US-10-067-477-2	US-08-796-570A-2	US-09-796-338A-16	US-09-897-201-1	US-09-796-338A-18	US-10-044-090-598	US-09-899-532-3	US-09-899-532-1	US-09-826-508-21	US-10-112-599A-3	US-10-101-487-76	US-10-101-487-74	US-09-905-186A-8	US-09-905-186A-7	US-09-940-240-19	US-09-880-107-3833	US-09-829-631A-9	US-09-829-631A-7	US-09-905-186A-1	US-10-044-090-627	US-10-044-090-628	US-10-090-569-11	US-09-905-186A-11	US-09-905-186A-10	US-09-905-186A-9
e 10	2	2, AJ	Sequence 16, Appl	Sequence 1, Appli	18, A	Sequence 598, App	ω	1, A	Sequence 21, Appl		76,	74,	Sequence 8, Appli	Sequence 7, Appli	Sequence 19, Appl	Sequence 3833, Ap	Sequence 9, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 627, App	e 628	Sequence 11, Appl	Sequence 11, Appl	Sequence 10, Appl	Sequence 9, Appli

#### ALIGNMENTS

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1257)
US-09-804-551B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09804551B
Patent NO. US20020056151A1
GENERAL INFORMATION:
APPLICANT: Bayer Aktiengesellschaft
TITLE OF INVENTION: Receptors for peptides
FILE REFERENCE: Le A 34 394
CURRENT APPLICATION NUMBER: US/09/804,551B
CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 25
LENGTH: 1258
TYPE: DNA
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                             Matches 241;
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
 234
                                                                                                                                            CTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAA 179
GTCCTACATCTGGTCCAAGTACCCGTACGTGTTTGGGGGAGTACATCTGCATCGGACGTGG
                     CTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGAC
                                                                     CCTCTTTTCGCTGGCCATCTCGGATTTCCTGCTCGTGTTGTCGGGGGGTTCCGCAGGAGGT
                                                                                                          CCTCTTCAGCCTGGCCGTCTCTGACCTCCTGGTCCTTGCTCCTTGGAATGCCCCTGGAGGT
                                                                                                                                                                                                                      CATCGTGATACCCGTAACGGTGGTCTACTCCCTCATTTTCATAACCGGTGTAGTGGGCAA
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                                                                                                                                                                                                                                                                                                               16.48;
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Pred. No. 1.9e-21;
Prematches 202;
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Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using SignaturiTLE OF INVENTION: Sets

FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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                 GGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCATGGCATCA
                                                                       CTCTGCGCGCGGCGACCTACCGGCGGCCCAGCGTGGCCAAGCTCATCAACCTGGGCGTGT
                                                                                                                                                                                  TCGCCTCCATCCTCAGCATCACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACC 442
                                                                                                                                                                                                                                                                                                                                                                                                 TGCAGCAGCAGGCTATGAAGACGCCCACCACTACTACCTTTCAGCCTGGCGGTCTCTG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAATGTCCTGGTGTGTGCCTGGTGATTC 202
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                                                                                                                                                 TCACCAGCGTCTTCTGTCTCACCGTGCTCAGCGTGGACCGCTACGTGGCCGTGCTGCACC
                                                                                                                                                                                                                           C----CTTCGGCTCCGTGCTGTGCCGCGCGGTGCTCAGCGTCGACGGCCTCAACATGT
                                                                                                                                                                                                                                                              CTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTGTGCT
                                                                                                                                                                                                                                                                                                  ACGAGCTCTTCATGCTGAGCGTGCCCTTCGTGGCCCTCGTCGGCCGCCCTGCGCCACTGGC 435
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                                                                                                                                                                                                                                                                                                                                       ACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTCTATGAGATGTGGCGCAACTACC 322
                                                                                                                                                                                                                                                                                                                                                                            TTCGCTACGCCAAGATGAAGACGGCTACCAACATCTACCTGCTCAACCTGGCCGTAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTACGCGCTGGTGTGCCTGGTGGGGCCTGGTCGACGCCCTGGTCATCTTCGTGATCC 315
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Pred. No. 1.4e-14;
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APPLICANT: XI, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSTS OF OVARIAN C:
FILE REFERENCE: 210121.484C5
CÜRRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 208
LENGTH: 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
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P.
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                                                                                         OVARIAN CANCER
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610 GGCTGGCATCCCTGTTGGTCACTCTCCCCATCGCCATCTTCGCAGACACCA 660
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

164 TGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGA 223 CGCCCACCAACTACTTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTTCCTTG 283 GCATGCCCATGGAGTTCTACAGCATCATCTGGAATCCCCTGACCACGTCCAGCTACACCC GAATGCCCCTGGAGGTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGC----CCG 340 TGTCCTGCAAGCTGCACACTTTCCTCTTCGAGGCCTGCAGCTACGCTACGCTGCACG TGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCA 400 TGGGGAACAGCGCCACCATTCGGGTCACCCAGGTGCTGCAGAAGAAAGGATACTTGCAGA 196 AGGAGGTGACAGACCACATGGTGAGTTTGGCTTGCTCGGACATCTTGGTGTTCCTCATCG Mismatches 166; Length 1362; Indels Gaps 460 256

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for Windows Version

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Query Match
Best Local Similarity
Matches 200; Conserva
                                                                                                         : LOCATION: (135)...(1454)
: NAME/KEY: misc_feature
: LOCATION: (1)...(1647)
: OTHER INFORMATION: n = A,T,C
US-09-829-631A-12
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                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/829,631A CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 08/428,242
PRIOR FILING DATE: 1995-09-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LECTURE 14.7
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09829631A
Patent No. US20020091235A1
EMERAL INFORMATION:
APPLICANT: Sibley, David R.
APPLICANT: Monsma, Frederick J.
APPLICANT: Hamblin, Mark
TITLE OF INVENTION: The ST-B17 Serotonin Receptor
FILE REFERENCE: NIH047.1CPLC1
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SEQ ID NO 208
LENGTH: 1362
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Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                          TYPE: DNA
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158 TTGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTA 217
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                                Score 85.6; DB 10;
Pred. No. 1.1e-12;
0; Mismatches 169;
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                                                                  US-09-917-800A-1620
                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1620
LENGTH: 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1620, Application US/09917800A Patent No. US20020119462A1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/917,80 CURRENT FILING DATE: 2001-07-31 PRIOR APPLICATION NUMBER: US 60/222,040 PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR APPLICATION NUMBER: US 60/222,880 PRIOR FILING DATE: 2000-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
                                                                                                             FEATURE:
                                                                                                                             ORGANISM: Rattus norvegicus
                                                                                                                                                      TYPE: DNA
                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598
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                                                                                                                                                                                                                                                                                                                                              OR APPLICATION NUMBER: US 60/290,645
OR FILING DATE: 2001-05-15
OR APPLICATION NUMBER: US 60/292,336
OR FILING DATE: 2001-05-22
OR APPLICATION NUMBER: US 60/295,798
OR FILING DATE: 2001-06-06
OR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCTCCCTGC 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCCTCCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAAGACGCCCACCAACTACCTACTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCATGACGCCCTGCGTGCCCTGGCCCTAGTCCTGGGCGGCTGGAGCCTCGCCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson, Kory
Castle, Arthur
Elashoff, Michael
                                                                                    Genbank Accession No. US20020119462A1 NM_016991
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11.3%;
47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/09/917,800A
Score 82.6; DB 10; Pred. No. 7e-12;
                  Length 2108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457
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Matches

278;

149

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; LOCATION: (1)..(1341) ; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein US-10-077-870-1
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10077870 Publication No. US20030003470A1 GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/077,870 CURRENT FILING DATE: 2002-05-21 PRIOR APPLICATION NUMBER: FI 20010323 PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Salonen, Jukka T TITLE OF INVENTION: Method for detecting a FILE REFERENCE: 0933-0183P
  170 TCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 GAAAGAACCTGCGCCCAATGATGACAAAGAATGTGGGGTCACCGAAGAACCCTTCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 TGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 GATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCCTGCCCAACACCAGCATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 CATTGGGGTGCGATACTCTGCAGTACCCCCACGCTGGTCACCCGCAGGAAGGCCATCTT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGC 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGGTCTACATCGTGGCCAAGAGGACCACCAAGAATCTGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGGCCATCCTACACCCGTTCCGCGCCCAAACTGCAGAGCACCCGGGCGCGCGGGCCCTCAG 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCTGGCGGTCTCTGACCTCCTGGTCCTTGCTTGGAATGCCCCTGGAGGTCTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGCGCTA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAGTGCTTGGCTACTGGGTGCTGTTGAGTTTCTT---CTGTGACATCTGGGCAGCGGT
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                                                                        Conservative
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                                                                                       Score 82; DB 9;
Pred. No. 8.5e-1;
                                                                     Mismatches
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                                                                     185;
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                                                                                                           Length 1344
                                                                   Indels
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                                                                                                                                                               ; LUCATION: (1)...(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
    DЬ
                                         QΥ
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US-09-825-923-1
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                                                                                       Matches 206;
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09825923 Patent No. US20010016338A1
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: U9/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION UMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Snapir, Amir APPLICANT: Heinonen, Pa
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          LENGTH: 1344
                        170 TCATTGGCAATGTCCTGGTGTGCCTGGTGAATTCTGCAGCACCAGGCTATGAAGACGCCCA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 CCCTGGAGGTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGGTGGGCTGCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
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CGCCCCTCATCTACAAGGGCGACCAGGGCCCCCA 470
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Karvonen, Matti
Koulu, Markku
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Nyyss"nen, Kristiina
Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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                                                                                     Conservative
                                                                                                      11.2%;
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                                                                                                      Score 82; DB 10;
Pred. No. 8.5e-12;
                                                                                   Mismatches
                                                                                                                          Length 1344;
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                                                                              Gaps
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US-10-077-870-1

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Query Match Best Local Similarity

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TYPE: DNA
ORGANISM: Homo NAME/KEY: CDS FEATURE:

sapiens

LENGTH: 1344

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Sequence 3, Application US/10077870

Publication No. US2003003470A1

GENERAL INFORMATION:

APPLICANT: Salonen, Jukka T

TITLE OF INVENTION: Method for detecting a ri:
FILE REFERENCE: 0933-01839

CURRENT APPLICATION NUMBER: US/10/077,870

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: HI 20010323

PRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10
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NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein US-10-077-870-3
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US-10-077-870-3
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Best Local Similarity
Matches 206; Conserv
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TYPE: DNA
ORGANISM: Homo sapiens
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                                    TCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCC
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                                                                                                                                                     CTTTCTCGCTGGCCAACGAGCTGCTGGGCTAC---TGGTACTTCCGGCGCACGTGGTGCG 256
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TCAGCCTGGACCGCTACTGGGCCGTGAGCCGCGCGCTGGAGTACAACTCCAAGCGCACCC
                                                                          AGGTGTACCTGGCGCTCGACGTGCTCTTCTGCACCTCGTCCATCGTGCACCTGTGCGCCA 316
                                                                                                              ACTICAAGACGGCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCG 409
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; 52.3%;
                                                                                                                                                                                                                                                                                                                                                                                      Score 82; DB 9; Louis Pred. No. 8.6e-12; 0; Mismatches 185;
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US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
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LENGTH: 1353
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding se
OTHER INFORMATION: protein
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Best Local Similarity
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APPLICANT:
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: A protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/422,985
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                             170 TCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCA 229
     317
                                   410 TCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCC 469
                                                                                                                                                                                                            140
                                                                                                                                                                                                                           230 CCAACTACTACCTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGC 289
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                                                                                                                                                                        CCCTGGAGGTCTATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCT 349
                                                                                                                                                                                                          AGAACCTGTTCCTGGTGTCGCTGGCCGCCGCCGACATCCTGGTGGCCACGCTCATCATCC
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                                                                                                                                                                                                                                                                           INFORMATION:
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Nyyss"nen, Kristiina
Salonen, Riitta
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Alhopuro, Pia
Karvonen, Matti
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Salonen, Jukka T
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                                                                                                                                                                                                                                                                                                                                                             DB 10;
8.6e-12
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CURRENT FILING DATE:

2002-01-18

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US-10-044-090-444
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        GENERAL INFORMATION:
APPLICANT: Perez, Dianne
APPLICANT: Zuscik, Michael
APPLICANT: Zuscik, Michael
TITLE OF INVENTION: Model systems for neurodegenerative and cardiovascular disorders
FILE REFERENCE: 26473/04200
                                                                                                   Sequence 1, Application US/10052589 Patent No. US20020133832A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES [
FILE REFERENCE: PA-0028 US
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    CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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  NUMBER:
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52.2%;
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US/10/052,589
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Pred. No. 6.2e-11;
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FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR APPLICATION NUMBER: US/60/236,028
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                                                                                                                                                                                                                                              Sequence 249, Application US/09964824A Patent No. US20020102531A1 GENERAL INFORMATION:
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LENGTH: 2048
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TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
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nes 275; Conserv
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Pred. No. 1.
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                                                          ; NAME/KEY: CDS
; LOCATION: (91)..(1176)
US-09-940-240-15
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                                                                                                                                                                        NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15
LENGTH: 2050
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SOFTWARE: PatentIn version
SEQ ID NO 249
LENGTH: 2595
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Best Local Similarity
  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: MBIO98-008CD1CN1M
CURRENT APPLICATION NUMBER: US/09/940,240
CURRENT FILING DATE: 2001-08-27
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/248,239
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 09/023,664
PRIOR FILING DATE: 1998-02-08
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NEOKINE PROTEIN AND TITLE OF INVENTION: THEREFOR
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OTHER INFORMATION: n=a,t,g
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                                                                                                                                    ORGANISM: Homo
                                                                                                                                                          TYPE: DNA
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                                                                                                                    FEATURE:
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US-09-954-531-995
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                                                                                                                                                                                                                                                                                                                                               Sequence 995, Application US/09954531 Patent No. US20020165180A1
SOFTWARE: PatentIn version SEQ ID NO 995
                                                PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Process for Identifying TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77
                                   NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/234,009 PRIOR FILING DATE: 2000-09-20
                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/233,133 PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/954,531
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Search completed: January 17, 2003, 02:36:32 Job time: 70 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
5: sp_manmal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Match
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1263
1 MEKLQNASWIYQQKLEDPFQ.....LLPMTVISVLYYLMALRVSI
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     Maximum Match 100%
Listing first 45 summaries
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sp_vrodent:*
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sp_invertebrate:*
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   DВ
     Q9GZQ4
Q96AM5
Q96AM5
Q9ESQ4
Q9ESQ4
Q9JIB1
Q9HB89
Q9JIB2
Q9JJI5
Q9JJI5
                     Q9VFW6
Q9VFW6
Q9VFW5
Q18701
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Q9gzq4 homo sapien Q96am5 homo sapien Q91z76 mus musculu Q9esq4 rattus norv Q9jib1 rattus norv Q9jib2 rattus norv Q9jib2 rattus norv Q9jji5 rattus norv Q9ji5 rattus norv Q9ji5
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17
243	243	243	243.5	244	246	248	4	250.5	252.5		253	253.5	255	255	255	255	255	255	255	256	256.5	257	257.5	259	277	281		295
19.2	19.2	19.2	19.3					•						•							•			20.5	•		•	23.4
443	414	414	390	370	513	431	404	395	356	346	383	454	444	438	409	401	393	391	390	410	377	464	400	401	416	416	559	397
6	6	6	13	13	13	σ	13	S	4	4	13	4	11	11	11	11	11	11	11	4	13	ഗ	9	13	11	11	13	13
Q9GJU1	Q9GK99	Q9GKA0	Q8QGQ4	Q8UWL5	Q9DFA9	Q8T8D1	Q9DFB0	Q95YD7	Q96TF2	Q96GE0	042324	Q9н573	Q9JIY1	Q9R0D1	Q8VI69	Q9R1L9	Q9R1M0	Q8VI70	Q8VI71	Q8TBH6	Q98U14	Q9GQ54	Q95M54	Q9DDR0	Q8VIF5	Q920Q5	093414	Q9DDR1
	Q9gk99 canis famil		Q8qgq4 carassius a	Q8uw15 fugu rubrip	Q9dfa9 catostomus	Q8t8d1 urechis uni	Ō	caen	Q96tf2 homo sapien	Q96geO homo sapien	cato	Q9h573 homo sapien	Q9jiy1 mus musculu	Q9r0d1 mus musculu	Q8vi69 mus musculu	Q9r119 mus musculu	Q9rlm0 mus musculu	Q8vi70 mus musculu	Q8vi71 mus musculu		Q98ul4 brachydanio	Q9gq54 aedes aegyp		Q9ddr0 xenopus lae	Q8vif5 mus musculu		093414 sphoeroides	Q9ddrl xenopus lae

## ALIGNMENTS

RP RA	RT RT	RP RA	AC REGERAL SOOO OO O	RESULT Q9GZQ4 ID Q
SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Pang L., Wang S., Laz T., Hedrick J.A.;  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  [4]  SEQUENCE OF 4-415 FROM N.A.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Shan L., Qiao X., Crona J.H., Behan J., Wang S., Laz T., Bayne M.,  Shan L., Qiao X., Crona F.J. Jr., Hedrick J.A.;  "Identification of a Novel Neuromedin U Receptor Subtype Expressed in the Central Nervous System.";  J. Biol. Chem. 275:39482-39486(2000).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE=20490668; PubMed=10899166; Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A., Borowsky B., Raddatz R., Wilson A.E., Kouranova E.V., Nagorny R., Guevarra M.S., Boteju L.W., Zhou S., Kouranova E.V., Nagorny R., Gerald C., Forray C., Dai M., Lerman G.S., Vaysse P.J., Branchek T.A., Gerald C., Forray C., Adham N.; "Identification and Characterization of Two Neuromedin U Receptors Differentially Expressed in Peripheral Tissues and the Central Nervous System."; J. Biol. Chem. 275:32452-32459(2000).	Ol-MAR-2001 (TrEMBLrel. 16, Created) Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update) Ol-MAR-2001 (TrEMBLrel. 21, Last annotation update) Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update) Neuromedin U receptor 2 (Neuromedin U receptor-type 2) (G protein-coupled receptor TGR-1). NMUR2 OR NMU2R OR TGR-1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID-9606;	JLT 1 204 205204 PRELIMINARY; PRT; 415 AA.

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Best Local :
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Q96AM5;
Q96AM5;
O1-DEC-2001 (TrEMBLrel. 19
O1-DEC-2001 (TrEMBLrel. 19
O1-JUN-2002 (TrEMBLrel. 2)
Neuromedin U receptor 2.
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; BC016938; AAH16938.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; pF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01567; NEUROMEDNUR.

PRINTS; PR01570; NEPFERCEPTOR.

PRINTS; PR01570; OPFFRCEPTOR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuromedin U Receptor.";
J. Biol. Chem. 275.29528.29532(2000).
EMBL; AF272363; AAG24794.1; -.
EMBL; AF292402; AAG03064.1; -.
EMBL; AF242874; AAF82755.1; -.
EMBL; AB04128; BAB13721.1; -.
                                                                                                    TISSUE=COLON;
                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Shintani Y., Fukusumi S., Habata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujino M.;
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Last annotation updat
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                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Best Local
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Best Local Similarity
Matches 238; Conserv
                                                                                                                                                                                           Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                      Gustafson E.L.;
"Characterization of murine neuromedin Submitted (SEP-2001) to the EMBL/GenBan EMBL; AY057384; AAL26695.1; -
InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01565; NEUROMEDINUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O91Z76
O91Z76;
PRELIMINARY;
PRT; 395 AA.
O91Z76;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                PRINTS; PR01567; NEUROMEDNU2R.

PRINTS; PR01570; NPFERECEPTOR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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SEQUENCE
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PRINTS; PR01570; NEUROMEDNUZR.
PRINTS; PR01570; NPFFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuromedin U receptor type Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                       Funes S., Hedrick J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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121
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                                      VLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLEGPVGCYFKT 120
                                                                                                         MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
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ALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
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                         LLVCLVIARHQTLKTPTNYYLFSLAVSDLLVLLLGMPLEVYELWHNYPFLFGPVGCYFKT
                                                                              MGKLENASWIH-----DSLMKYLNSTEEYLAYLCGPKRSDLSLPVSVVYALIFVVGVIGN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHGIKFHYFPNGSLVPGSATFTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRL
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                                                                                                                                      196;
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                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
                                                                                                                                                                                           395 AA;
                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47770 MW;
                                                                                                                                                                                           44844 MW;
                                                                                                                                                 82.3%;
81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.3%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                       Yang
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                                                                                                                                                   Pred. No. 4.
                                                                                                                                                              Score 1039.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 7.5
l; Mismatches
                                                                                                                                                                                           0BB540024566903D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30BFEDD706436AB9 CRC64;
                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                              R2 receptor.";
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                                                                                                                                    20; Indels
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Best Loc
Matches
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Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01567; NEUROMEDIVER.

PRINTS; PR01567; NEUROMEDIVER.

PRINTS; PR01570; NPFFRECEPTOR.

PROSITE; PS01237; G_PROTEIN_RECEP_F1_1; UN

PROSITE; PS01237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSESQ4;
01-MAR-2001 (TIEMBLIEL 16, C
01-MAR-2001 (TIEMBLIEL 16, L
01-JUN-2002 (TIEMBLIEL 21, L
G protein-coupled receptor TG
TGR-1.
                                                          09JIB1;
09JIB1;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuromedin U Receptor.";
J. Biol. Chem. 275:29528-29532(2000).
EMBL; AB041229; BAB13722.1; -.
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Hosoya M., Moriya T., Kawamata Y., O
Shintani Y., Fukusumi S., Habata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ESQ4
                                         Neuromedin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujino M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MGKLENASWIH-----DPLMKYLNSTEEYLAHLCGPKRSDLSLPVSVAYALIFLVGVMGN 55
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norvegicus (Rat)
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                                       (TrEMBLrel.) (TrEMBLrel.) (Treceptor 2.
                                                                                                      (TrEMBLrel.
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                                                                                                                                                PRELIMINARY;
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                                                             Last sequence update)
Last annotation updat
                                                                                                      Created)
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Sciurognathi;
                                                                                                                                                PRT;
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Hinuma S.,
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thi; Muridae; Murinae; Rat
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Best Local
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pfam; pF00001; 7tm_1; 1.
pratvrs; pR00237; GPCRRHODOPSN.
prints; pR01565; NEUROMEDINUR.
prints; pR01567; NEUROMEDIVAR.
prints; pR01567; NEPFRECEPTOR.
prints; pR01567; NPFFRECEPTOR.
prints; pR0157; NPFFRECEPTOR.
prosite; pS00237; G_PROTEIN_RECEP_F1_1; UN
pROSITE; pS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20490668; PubMed=10899166;
MEDLINE=20490668; PubMed=10899166;
Raddatz R., Wilson A.E., Artymyshyn R., Bonini J.A
Boteju L.W., Zhou S., Kouranova E.V., Nagorny R.,
Boteju L.W., Zhou S., Vaysse P.J., Branchek T.A., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; (
Mammalia; Eutheria; F
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                  O9HB89; O43664;
O1-MAR-2001 (TERMBLrel. 16, Created)
O1-MAR-2001 (TERMBLrel. 16, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neuromedin U receptor 1 (Orphan G protein-coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY:
MEDLINE-20351041; PubMed=10894543;
HOWART A.D., Wang R., Pong S.-S., Mellin T.N., Strack A., Guan X.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy B.,
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mckee K.K.,
Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austin C.P.,
Caskey T., van der Ploeg L.H.T., Liu Q.;
"Identification of receptors for neuromedin U and its role in
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                       Differentially System.";
                                                                                                                                                                                                                                                                                       Q9нв89
                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
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                                                   "Identification
                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
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             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVVGVIGN
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                                                                                                                                                                                                                                                                                                                                                       IHGIKFQHFPNGSSVPGSATCTVTKPMWVYNLIIQATSFLFYILPMTLISVLYYLMGLRL
                                                                                                                                                                                                                                                                                                                                                                                                         ALFETVCFASTLSVTTVSVERYVAIVHPFRAKLESTRRRALRILSLVWSFSVVFSLPNTS
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AF242875; AAF82756.1;
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                     Expressed
             275:32452-32459(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                   Characterization
                                                                                                                                                                     Primates;
                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                     Peripheral Tissues
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Pred. No. 1.6
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                                                                                                                                                                    Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01D3765B5D5355C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                   of
                                                                                                                                                                                                                                                                                        426
                                     Two Neuromedin
                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN_1.
                                                                                                     Bonini J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6e-88;
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                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                           Gerald C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                         Guevarra M
                                                                                                                                                                                                                       receptor)
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                                                                                                       Borowsky
                                                   a
                                        Central Nervous
                                                   Receptors
                                                                             Forray
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                                                                                                                                                                                                                                                                                     102
109JIB2
29JIB2;
01-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-JUN-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; pF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHOODPSN.

PRINTS; PR01565; NEUROMEDINUR.

PRINTS; PR01566; NEUROMEDNUIR.

PRINTS; PR01570; NPFFRECEPTOR.

PRINTS; PR01570; NPFFRECEPTOR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UN

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                              MEDLINE=20351041; PubMed=10894543;
Howard A.D., Wang R., Pong S.-S., Mellin T.N., Strack A.,
Zeng Z., Williams D.L., Feighner S.D., Nunes C.N., Murphy
Stair J.N., Yu H., Jiang Q., Clements M.K., Tan C.P., Mcke
Hreniuk D.L., Mcdonald T.P., Lynch K.R., Evans J.F., Austi
Caskey T., van der Ploeg L.H.T., Liu Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
EMBL; AF242873; AAF82754.1; ...
InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
                                                                                   Caskey T., van der 
"Identification of
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 52:223-229(1998).
EMBL; AF272362; AAG24793.1; -.
EMBL; AF044601; AAC02680.1; JOINED
                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF044601; AAC
EMBL; AF044600; AAC
HSSP; P02699; 1F88.
                                                        Nature
                                                                        reeding."
                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-coupled receptor similar to the growth hormone secretagogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tan C.P., McKee K.K., Liu Q., Palyha O.C., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D., "Cloning and characterization of a human and murine T-cell orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99000845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 24-426 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPFOKHLNSTEEYLAF-LCGPRRSHFFLPVSVVVVPDIFVVGVIGNVLVCLVILQHQAMKT
                                                                                                                                                                                                                                                                                                                                                                                                                                         PDSAVCMLVRPRALYNMVVQTTALLFFCLPMAIMSVLYLLIGLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTNYYLFSLAVSDLLVLLVGLPLELYEMWHNYPFLLGVGGCYFRTLLFEMVCLASVLNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFASILSIT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DP--EDLNLTDEALRLKYLGPQQTELFMPICATYLLIFVVGAVGNGLTCLVILRHKAMRT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126;
                                                        406:70-74(2000)
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                                                                                    receptors
                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47350 MW;
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56.0%;
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21,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                          Clements M.K., Tan C.P., Mckee K.K.,
Lynch K.R., Evans J.F., Austin C.P.,
T., Liu Q.;
                                                                                   for neuromedin U and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 680.5; DB 4
Pred. No. 1.5e-55;
2; Mismatches 54
                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F8DD781C020F04AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Q9 Q9
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DR
DR
SQ
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                                                                                                                                     Query Match
Best Local :
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JJI5
Q9JJI5;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                                                         Receptor.
SEQUENCE
                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDIUUR.
PRINTS; PR01566; NEUROMEDRUULR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                  Fujii R., Hosoya M., Fukusumi S., Kawan Onda H., Nishimura O., Fujino M.; "Identification of neuromedin U as the protein-coupled receptor FM-3."; J. Biol. Chem. 275:21068-21074(2000). EMBL; AB038649; BAA99387.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                             Fujii R.,
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDNUIR.
PROSITE; PS00237; O_PROTEIN_RECEP_F1_1; UNKNOWN_1
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20347213; PubMed=10783389;
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
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                                                                                    SILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYF 189
                        QKAMHTPTNFYLFSLAVSDLLVLLVGLPLELYEMQHNYPFQLGAGGCYFRILLLETVCLA 134
                                     HQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYPFLFGPVGCYFKTALFETVCFA 129
                                                                       DSEFKEHFDLEDLNLTHEDLRLKYLGPQQVKQFLPICVTYLLIFVVGTLGNGLTCTVILR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYF
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                                                                                                                                     Similarity
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                                                                                                                                                                         412 AA;
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                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                                                         46784 MW;
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Rodentia;
                                                                                                                                   50.8%;
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54.1%;
                                                                                                                         36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                        Score 642; DB
Pred. No. 5.8e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation
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Pred. No. !
                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                         2CAB56299E2EA7B8 CRC64;
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5.7e-52;
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                                                                                                                                     .8e-52;
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RESULT
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Best Local :
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PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01565; NEUROMEDNUIR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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01-JUN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Orphan G protein-coupleo
                                                                                                                                                                                                                                                           Q9VFN4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McKee K.K., Tan C.T., Liu J., Palyha O.C., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF044602, AAC02681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                  01-MAY-2000
01-JUN-2002
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                           Ephydroidea;
                                                      Pterygota;
                                                                                    Eukaryota;
                                                                                                                Drosophila
                                                                                                                                                 CG9918
                                                                                                                                                                                                                                                                                                                        Q9VFN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1341898; Gpr66.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPYQP--ED-----LNLTDEALRLKYLGPQQMKQFVPICVTYLLIFVVGTLGNGLTCTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIYQQKLEDPFQKHLNSTEEYLAF-LCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASVLNVTALSVERYVAVVRPLQAKSVMTRAHVRRMVGAIWVLATLFSLPNTSLHGLSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FASILSITTVSVERYVAILHPERAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFH 187
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                           melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
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50.68;
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Last annotation updat
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Pred. No. 1
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F1BA493D3EB81F34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                     428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RX MEDLINE-2019606; PubMed=10731132;

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,

RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,

RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA McIkulov G., Mulshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacche J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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SEQUENCE FROM N.A.
STRAIN-BERKELEY;
STRAIN-70196006; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; ABO03703; AAF55016.1; -.
Flybase; FEB90038201; C59918.
InterPro: IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR0037; GPCRRHODOPSN.
PRINTS; PR0037; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 428 AA; 47198 MW; 9DD4A1E93046B6D7 CRC64;
                        213 IIQVTSFLFYLLPMTVISVLYYLMALRV
                                                                                 131
                                                                                                                                        153
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                                                                                                                                                                                                                                                                                                                                                                         GPRRS--HFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVL
                                                                                 AMSKLSRAIRIIVLVWIMAIVTAIPQAAQFGIE-HY-
                                                                                                                                        LQSTRRRALRILGIVWGFSVLFSLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNF
                                                                                                                                                                                               LSGVPQEVSYIWSKYPYVFGEYICIGRGLLAETSANATVLTITAFTVERYIAICHPFLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 40.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.1%;
40.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 418;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RA Addams N.D., Cclinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Cclinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Galeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., M.
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Diegwan C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Diegwan C.,
RA Harris N.L., Mattei B., McIncosh T.C., McLeod M.-H., Dogwan C.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Menter E.C., Steden Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Ranger E.C., Steden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R., Dect. Scheeler F., Shen H.,
RA Ranger E.C., Steden K., Weinstock G.M., Weissenbach J.,
Wallsam D.A., Weinstock G.M., Weissenbach J.,
Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Holliams S.M., Woodsey G., Shen M., Strong G., Zhou X., Smith H.O.,
Park Man S., Shen H., C., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q9VFW6
InterPro; ...
InterPro; IPR000z,,
InterPro; IPR0001; 7tm_1; 1.

Pfam: PF00001; 7tm_1; 1.

PFAm: PF000237; GPCRHODOPSN.

R PRINTS; PR01565; NEUROMEDINUR.

AR PRINTS; P800196; COPPER_BLUE; UNKNOWN_1.

DR PROSITE; P800237; G_PROTEIN_RECEP_F1_1; 1.

PS50262; G_PROTEIN_RECEP_F1_2; 1.

PS50262; G_PROTEIN_RECEP_F1_2; 1.

PS50262; G_PROTEIN_RECEP_F1_2; 1.

PS50262; G_PROTEIN_SECREPT12; 1.
                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0038139; CG8795.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO FAMILY EMBL; AE003699; AAF54929.1; -.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
^-Αγντανναοτα; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
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Last annotation update)
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RESULT
Q9VFW5
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                                                                                                                                                                                                                                                                                                                                             RA Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Mananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S.S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Babil J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gebbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Guzan G., Harris M.,
RA Harris N., Hayrey D. Heiman M., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                Shue B.C.,
Spier E., S
                                                                                                Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Mushina N.V., Mobarry C., Morris J., Moshrefi A.,
Wount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Chino B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VFW5;
Q9VFW5;
01-MAY-2000
                       Wang Z.-Y.,
                                         Svirskas R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMW 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLPMTVISVLYYLMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIFAIWIAALLLALP----QAIQFSVVMQGM----GTSCTMKNDFFAH--VFAVSGFLFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVGYALIFIAGVLGNLITCIVISRNNFMHTATNFYLFNLAISDMILLCSGMPQDLYNLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                       , Siden-Kiamos I., Simpson M., Skupski M.P., Sm
Spradling A.C., Stapleton M., Strong R., Sun E
R., Tector C., Turner R., Venter E., Wang A.H.,
                    Wassarman D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
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13,
21,
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Worley K.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                    Weinstock G.M., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
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Wu D.,
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.5e-25;
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                                                           Sun E.,
                                                                                  Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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RESULT 13
Q18701
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Best Local
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                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (Trem
01-NOV-1996 (Trem
01-JUN-2002 (Trem
C48C5.1 protein.
C48C5.1.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                              Q18701
Q18701;
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PRINTS; PR01365; GDERNEDINUR.
PRINTS; PS01565; REUROMEDINUR.
PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_3; Transmembrane.

G-PROTEIN_RECEP_F1_3; G-PROTEIN_RECEP_F1_3; Transmembrane.

G-PROTEIN_RECEP_F1_3; 1.
                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL, AE003699; AAF54930.1;
-Elybase; FBgn0038140; CG8784.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000923; BlueCu_1.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPFQKH----LNSTEEYLAFLCG-------PRRSHFFL--PVSVVYVPIFVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFLTHVAHLLNITTENLSNLLGSTNGTNASTMAADSPVDESLTLRTALTVCYALIFVAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPQAMQFSVVYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVISVLYY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLGNLITCIVISRNNEMHTATNEYLENLAVSDLILLVSGIPQELYNLW--YPDMYPFTDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLEVYEMWRNYP--FLFGPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295
                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.7%;
34.1%;
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01,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 337;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang G., Zhao
X., Zhu S., Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
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RESULT
017239
  В
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Best Local S
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                                                                                                                                                                                                                        01-JAN-1998
01-JAN-1998
01-JUN-2002
                                                                                                                                                                                                                                                           017239
017239;
                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PROSITE; PS000237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50062; G_PROTEIN_RECEP_F1_2;
SEQUENCE 378 AA; 43631 MW; 458DC60CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The sequence of C. elegans
                                                                                                                                                                                                  Hypothetical K10B4.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                     STRAIN-BRISTOL N2;
                                  SEQUENCE FROM N.A.
                                                           Science
                                                                                                       STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                    STRAIN-BRISTOL
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1995)
                                                          investigating biology. The C.
Science 282:2012-2018(1998).
                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium
                                                                                             None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Favello A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                              123
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                                                                                                                                                                                                                                                                                                                                  243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QKHLNSTEEY---LAFLCGPRRSH-------FFLPVSVVYVPIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPMTVISVLYYLMALRVS
                                                                                                                                                                                                                                                                                                                                                                                                                           YICNLKALIAETTSSVSILTILIFAIERYVAVCHPLFLMKVQPFKRNIGTIIGFTWIFSI 182
                                                                                                                                                                                                                                                                                                                                 ALPLFTIVILYARIACKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGCYFKTALFETVCFASILSITTVSVERYVAILHP-FRAKLQSTRRRALRILGIVWGFSV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVGVIGNTTTCLVMKKHPMMKTHASMYLMNLAVSDLVTLCVGLPFEVMMNWNQYPWPFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QACLNTTEDQCDCLAFNCPIVYSHSESEKEACYMEHCFISKRALDDVTLYKVTALYIFIF
                                                                                                                                                                                                                                                                                                                                                                               LCAMPFAIHHRADYIMKSWPGTDNRIPVKSSKMCMIAVMFEPKLASTFKILFHFSAIAFF
                                                                                                                                                                                                                                                                                                                                                                                                    LFSLPNTSIHGIKF -- HYFP -- - NGSLVPGSATCTVI -- -- KPMWIYNFIIQVTSFLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOV-1996)
                                                                                                                                                                                                            3 (TremBLrel. 05, Cre
3 (TremBLrel. 05, Las
2 (TremBLrel. 21, Las
al 47.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans

i) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.3%;
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                                                                                                                                                                                                                                                                                                                                                        241
          Antoniou
                                                                                                                                                               oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cosmid C48C5.";
EMBL/GenBank/DDBJ databases
 cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 332.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.1e-23;
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458DC60CCBF88F86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
 B.;
K10B4.";
                                                                                                                                                                                                                                                                       418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                          Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                      Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              242
                                                                                                                                                                                                                                                                                                                                                                                                     222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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6,

Submitted (SEP-1997)

to

the EMBL/GenBank/DDBJ databases.

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RESULT 15
093412
ID 09341
AC 09341
DT 01-N0
DT 01-N0
DT 01-JU
DE Orpha
OS Sphoe
OC Eukarr
OC Actir
Acant
           DЪ
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Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Hr
Gao Y.D., Schleim K.D., Yang L., Morriello G.J., Nar
Patchett A.A., Howard A.D., Smith R.G.;
"Ligand activation domain of human orphan growth hor
secretagogue receptor (GHS-R) conserved from pufferf
Mol. Endocrinol. 14:160-169(2000).
EMBL; AF082209; AAC33472.1;
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000524; HTH_GntR.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                          PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01565; NEUROMEDINUR.
PRINTS; PR01566; NEUROMEDNUIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Orphan G protein-coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sphoeroides nephelus.
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                093412
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 418 AA; 47735 MW; CE0416539CA3BB27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR01565; NEUROMEDINUR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF025463; AAB71009.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1...
     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 FERWLAICHPLRSKIFSTLWRANVLIILAWTISFVCALPIAFIVQINKLPLPEDAKYQPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 IVIMYAHIAVQL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 VERYVAILHPFRAKLQSTRRRALRILGIVWGFSVLFSLPNTSIHGI---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 YLFSLAVSDLLVLLLGMPLEVYE-MWRNYPFLFGPVGCYFKTALFETVCFASILSITTVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 HLNSTEEYLAFLCGPR--RSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISVLYYLMALRV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KFHYFP----NGSLVPGSAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNKVSFFAVGVLNNRIFPVSTDGIFVLHTEFCAMNQSRPDQQKMIIIFAFTVFFVIPAIA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLFSLAVSDIIALILGLPMEFYQSLDYSYPYRFSEGICKARAFLIEFTSYASIMIICCFS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVSEITEYVLSTLGERCQSAGIVIPTVIIYGTIFLLGLFGNICTCIVIAANKSMHNPTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sphoeroides.
G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%;
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Pred. No. 2.3e-20;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---CTVIKPMWIYNFIIQVTSF-LFYLLPMTV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
                                                                                                                                                                                                                                                                                    growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodontiformes;
                                                                                                                                                                                                                                                      pufferfish to humans.";
                                                                                                                                                                                                                                                                                                                                            Nargund
                                                                                                                                                                                                                                                                                                                                       Hreniuk D.L.,
Nargund R.,
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PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
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                                             CRMTQYAVESGLMEAMVWL - - - - -
                                                                       CTVIK------PMWIYNFIIQVTSFLFYLLPMTVISVLYYLMALRV
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6,

Search completed: January 17, Job time: 97 secs

GenCore version 5.1.3 Compugen Ltd

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Human GTP-binding	Human G protein co	Human orphan G pro	Nucleotide sequenc	Nucleotide sequenc	Human DNA for pote	Human DNA for pote	Human nGPCR15 codi	Nucleotide sequenc	Description		

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upled receptor PFI-002.  al transduction; diabetes; psychotherapy; dermatology; tissue repair; photoageing; cardiovascular disease; ergy; respiratory disease; air loss; gene therapy;				Human G protein co Genomic sequence o	TO C	eotide se	encoding	<b>H</b> (0)	Se c	G-protein	Rat G-protein coup	an G-protein c		DNA encoding human	Human G-protein-co	E	novel	Rat G-protein coup	leotide	CO.	Nucleotide sequenc	seq	plice variant	Splice variant of	NMURZ CONA.	n G-prot	Human G-protein co

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729; Conserv
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                                                                                       Schellin
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                            polynucleotide useful
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                                      protein-coupled
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                                                                                                Wood LS,
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                          and
                                                                                     h RR,
Ruff
                                     and its encoding
                           treating
                                                                                     Lind P, Slightom V, Sejlitz T, Hui
                          e.g. schizophrenia
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Claim

Page

78-79;

261pp; English

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Screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for dentifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or clistorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular clistorders, infections such as HIV-1, metabolic and cardiovascular clistorders, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's crespiratory allments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 729;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 801 BP; 200 A; 187 C; 261 G; 153 T; 0 other;
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TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
                                                                          TGTACGGTCATCAAGCCCATGTGGATCTACAATTTCATCATCCAGGTCACCTCCTTACTA
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Pred. No. 4.1e-148;
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Human; G protein-coupled recep
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Acherosclerosis; basal cell ca
Chondrosarcoma; chronic obstru
XW
depression; epilepsy; macular
XX
Disnov-2001.
XX
Homo sapiens.
XX

11-MAY-2001; 2001WO-US15332.
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11-MAY-2000; 2000US-203217P.
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11-MAY-2000; 2000US-20321
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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polypucleotides included in the specification. CC Also included are probes based on the GPCR sequences (including comprising an expression vector comprising comprises probes), a host cell comprising an expression vector comprising comprises probes are useful comprising an expression vector comprising comprises and methods of identifying modulators of the polypeptides. The compression as modulators, activators, repressors, agonists or antagonists of inction as modulators, activators, repressors, agonists or antagonists compression as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GALA polypeptide. The compression and nucleic acid probes as described above can be used to diagnose a variety of diseases or disorders in which GPCRs are involved ceg. Alzheimer's disease, amyotrophic lateral sclerosis, asthma, cardiomyopathy, compression, epilepsy, macular degeneration, lymphoma, melanoma, complete sclerosis, osteoarthritts, osteoporosis, parkinson's disease, complete sclerosis, osteoarthritts, schizophrenia, ulcerative colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obesity; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes; hyperlipidaemia; stroke; gene therapy.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                  TTCTACCTCCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
                                                                   TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
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Pred. No. 4.1e-148;
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Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis, stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disea; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obesity; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2000;
18-MAY-2000;
Disclosure; Page 120-121; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes; hyperlipidaemia; stroke; gene therapy
                                                                                                                                                                                                                                                                                                                                                                  (LIFE-) LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                 Miller M,
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2000US-205945P
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                                                                                                                                                                                                                                                                                                     Burmer
                                                                                                                                                                                                                                                                                                 G,
                                                                                                                                                                                                                                                                                                 Fabre-Suver
                                                                                                                                                                                                                                                                                                 C,
                                                                                                                                                                                                                                                                                                 Pritchard
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CC The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polypucleotides included in the specification. CC Also included are probes based on the GPCR sequences (including cantisense probes), a host cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides. The C cand methods of identifying modulators of the polypeptides. The C cand methods of identifying modulators of the polypeptides. The C cantibodies and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acids and are used to cathorouse a variety of diseases or disorders in which GPCRs are involved ce.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, cardiomyopathy, conductors, polippsy, macular degeneration, lymphoma, melanoma, chronic obstructive pulmonary disease, Crohn's disease, or multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease, compressis, pain perception disorders listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory cdisorders, pain perception disorders, obesity, diabetes, Alzheimer's cdisorders, phyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the invention.

RESULT 4
AAS98055
ID AASS

AAS98055 standard;

DNA; 1239

QS

Sequence

1239

BP;

267

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RESULT 5
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                                                                                                 of a human TGR-1 protein
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99.7%;
                                                           hypertension;
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24-FEB-2000;
30-MAR-2000;
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of binding properties of neuromedin U to TGR-1. The method is useful for screening preventatives and remedies for hypertension, stress diseases, etc.. TGR-1 antagonists are also useful for treating the same diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying predicted or actual structures of two chemical or physical library by mass spectrometry correlating molecular mass measurements of two or shared chemical history .
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                                                                                                                                                                                                                                                                                                                            Sequence 1245 BP;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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DB; AAG63353.
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CGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCGGGCC
                  GCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
                           GCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
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2000JP-0052252.
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2000JP-0187536.
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43075
The present sequence encodes a human TGR-1 protein. The specification describes a method of screening a compound, which is capable of bindi properties of neuromedin U to TGR-1. The method is useful for screeni
                                                                                                                                      Identifying predicted or actual structures of two or more members chemical or physical library by mass spectrometry comprising correlating molecular mass measurements of two or more members with shared chemical history -
                                                                                          Disclosure; Page
                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000; 2000JP-0032773.
24-FEB-2000; 2000JP-0052252.
30-MAR-2000; 2000JP-0097896.
19-JUN-2000; 2000JP-0187536.
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screening

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protein-coupled receptor; GPCR; hRUP6; drug

screening;

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protein-coupled

receptor hRUP6 cDNA

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                                                                                                                                                                                                                                                                ATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACC
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189

120

69 60

129

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The present sequence is a cDNA encoding hRUP6, an endogenous human corphan G protein-coupled receptor (GPCR). The full length hRUP6 cDNA was cloned by RT-PCR using human thymus cDNA as template.

The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                Query Match
Best Local Similarity
Matches 719; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1998
11-FEB 1999
26-FEB 1999
112-MAR-1999
112-MAR-1999
28-MAY 1999
28-MAY 1999
28-MAY 1999
28-MAY 1999
28-MAY 1999
29-SEP 1999
29-S
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Pred. No. 1.2e
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669 660 609 600 549 540 489 480 429 420 369 360 309 300 249 240

pharmaceutical;

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29-SEP-1999;
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28-MAY-1999
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28-MAY-1999
                                                                                                                                                                                                                                                                                                                       The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46117 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1998;
12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
16-FEB-1999;
                                                                                                                                                                                                                                                                                        Sequence 1248 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents
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CTCTTCAGCCTGGCGTCTCTGACCTCCTGGTCCTTGCTTCGAATGCCCCTGGAGGTC
                                       GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGCCTATGAAGACGCCCACCAACTACTAC
                                                                                          TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGCCAAT
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                         GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCCACCAACTACTAC
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                                                                             TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT
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iaw CW, Lin I,
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tz K, White
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31-MAR-2000;
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                                                                                                                                                                                                          GTP-binding protein-coupled receptor; neuroprotective; immunomodulatory; muscular; urinary; circulatory; anorectic; gene therapy; human;
                                                        Sugiyama
                                                                  Matsumoto
                                                                                                                                                  05-JUL-2001.
                                                                                                                                                                   WO200148189-A1
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                  guanosine triphosphate;
                                                                                                                                                                                                                                  Human GTP-binding protein-coupled receptor GPRv39 coding sequence
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DB; AAG64297.
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2000JP-0101339.
2000JP-0155978.
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Family of guanosine triphosphate binding protein coupled receptors and genes encoding them for treatment and prevention of diseases associate with these receptors  $\,$ 

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htches 719; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1248
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99.7%;
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Pred. No. 1.7
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RESULT 10 ABK47909 ID ABK47

ABK47909 standard; cDNA; 1248

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fungal infection; protozoan infection; viral infection; hypertension; path; dlabetes; obesity; anorexia; bulimia; Parkinson's disease; stroke; acute heart failure; hypotension; urinary retention; osteoporosis; ulcer; angina pectoris; myocardial infarction; benign prostatic hypertrophy; allergy; migraine; vomiting; psychotic disorder; neurological disorder;
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P-PSDB; AAU77155.
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                        AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC 120
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                                                                                                              ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
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/product= "Human AXOR34"
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1..1248
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BEECHAM PLC.
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99.7%;
                                                                                                                                                                                                                          Score 717.8; DB 24;
Pred. No. 1.2e-145;
""cmatches 2;
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                                                                                                                                                                                                                                                                                                                                               318 T; 0 other;
                                                                                                                                                                                                                                                                                             24;
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                                                                                                                    Alzheimer's disease; AIDS; hormonal disorder; memory disorder; migraine; cardiovascular disorder; renal disorder; bone disease; delirium; asthma; Cushing's disease; dysmenorrhoea; antianginal; cytostatic; osteoporosis; metabolic disorder; behavioural disorder; Addison's disease; dyskinesia;
                                                                                                                                                                                             respiratory disorder; depression; schizophrenia; dementia; obesity; pain; gastrointestinal disorder; hypertension; hypotension; epilepsy; diabetes; ischaemia; stroke; cancer; sexual disorder; circadian disorder; anorexia;
                                                                                                                                                                                                                                         Human; G-protein coupled receptor; SNORF72; neuromedin U neuropeptide; NMU; inflammation; arthritis; autoimmune disease; septicaemia; psychotic; mental retardation; transplant rejection; neurological disorder; anxiety;
                                                                                                                                                                                                                                                                                                      Human G-protein coupled receptor, SNORF72 cDNA.
                                                                                                                                                                                                                                                                                                                                       07-AUG-2001
                                                                                                                                                                              dermatological; psoriasis; Parkinson's disease; nausea; bulimia;
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                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                       antiulcer;
                               Location/Qualifiers 27..1274
              /*tag=
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                                                                                                       antiaddictive;
"Human SNORF72 receptor"
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PR PR XXX
                                                                                                                                                                                                                 useful for treating various pathophysiological conditions such as clinical manufactor, arthritis, autoimmune diseases, transplant rejection, graft vs host disease, bacterial, fungal, protozoan and viral infections, compared to the protozoan and cardiovascular concers, and the protozoan and cardiovascular concers, and the protozoan and cardiovascular constatic hypertrophy, gastrointestinal disorders, nasal congestion, compared to prostatic hypertrophy, gastrointestinal disorders, nasal congestion, compared to prostatic hypertrophy, gastrointestinal disorders, angina disorders, consistent of disease, Alzheimer some and the protozoan and the protozo
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25-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human G-protein coupled receptors, SNORF62 and SNORF72 and their corresponding cDNA molecules. SNORF62 and SNORF72 receptors are specific for neuromedin U (NMU) neuropeptides, hence they are also known as NMU receptors. The agonist and antagonist of NMU receptors are useful for treating an abnormality in a subject that is alleviated by decreasing or increasing the activity of NMU receptor. The NMU receptors serves as a valuable tool for designing drugs which are
                                                                                                                            disorders, somatosensory disorders, metabolic disorders, behavioural disorders, drug addiction, migraine, Addison's disease, Cushing's disease, prevent miscarriage, induce labour or to treat dysmenorrhoea
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 42; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases, transplant rejection, AIDS, cancer -
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                                                                                                 The present cDNA sequence encodes human G-protein coupled receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A purified mammalian SNORF62 or SNORF72 receptor protein for identification of compounds to treat e.g. inflammation, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYNA-) SYNAPTIC PHARM CORP
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BP; 278 A; 405 C; 282 G; 333 T; 0 other;
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Ploeg
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            Howard
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              R,
                                                                                                        "Human
                                                                                                                                                                  NMUR2;
            Mellin
Tiang Q,
                                                                                                          NMUR2 protein'
                                                                                                                                                                  FM-4
              TN, Stra
Williams
                                                                                                                                                                 protein; eating;
                    A
                                                                                                                                                                 weight gain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                       720
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Query Match
Best Local s
Matches 719
                                                                                                                     The invention relates to human and rat neuromedin U receptor designated NMUR2 polypeptides and polynucleotides. NMUR2 also referred as FM-4, is free from associated proteins and is involved in the feeding behaviour in mammals. Sequences of the invention are useful for identifying compounds which modulate the feeding activity of a mammal. The compounds identified are useful for modulating eating and weight gain. The present sequence is human NMUR2 cDNA.
                                                                                                                                                                                                                                                                                                                                 New polypeptide, useful for identifying compounds feeding activity of a mammal, comprises the novel rat neuromedin U receptor designated NMUR2 -
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE14262
                                                                                     Sequence 1344 BP;
                                                                                                                                                                                                                                                                                              Example 1;
                         Similarity
                                                                                                                                                                                                                                                                                          Fig
        Conservative
                                                                                     291 A; 419 C; 290 G;
                                                                                                                                                                                                                                                                                            47pp;
                         98.5%;
                                                                                                                                                                                                                                                                                            English.
      0;
                       Score 717.8; DB Pred. No. 1.2e-1
        Mismatches
                                                                                     344 T; 0 other;
; DB 24;
1.2e-145;
2;
                                                                                                                                                                                                                                                                                                                                                          which modulate isolated human
        Indels
                                          Length
        0;
      Gaps
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                                                                                                                                          TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT
                                                                                                   CGCTACGTGGCCATCCTACACCCGTTCCGCGCCAAACTGCAGAGCACCCGGCGCCCGGGCC
                                                                                                                                                                                                                                    GCCCTCTTTGAGACCGTGTGCTTCGCCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
                                                                                                                                                                                                                                                                             TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
D
                                                           TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGCCCGTGGGCTGCTACTTCAAGACG
                                                                                                                                                                                                                                                                                                          CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCTGGAGGTC
                                                                                                                                                                                                                                                                                                                     CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTCCTTGGAATGCCCCCTGGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
                     TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGACTA
                               TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
                                                                                                                                                                                   CGCTACGTGGCCATCCTACACCCGTTCCGCGCCCAAACTGCAGAGCACCCGGCGCCGGGCC
                                                                                                                                                                                                                            GCCCTCTTTGAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAG
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AAZ33297
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                       DЬ
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                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human G-protein coupled receptor neurotensin-like receptor (NLR). The NLR polynucleotide and protein can be used to isolate compounds that bind, (ant)agonise or alter the activity or expression of the NLR. The NLR is a G-protein coupled receptor which is expressed in the central nervous system and shares homology with human neurotensin receptor. The receptors can be used in
                                                                                                                                                                                                                                                                                                                   Sequence 1360 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel neurotensin-like receptor, useful for identifying agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ahmad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09955732-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neurotensin-like receptor; NLR: G-protein coupled receptor; central nervous system; anasthesia; analgesia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ASTR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR-) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ33297 standard;
301
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                                                                                                                       194
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                                                                                                                                                                     134
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                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                           _
                                                                   ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                   CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTGCTCCTTGGAATGCCCCCTGGAGGTC
                                                                                                                               TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT 180
                                                                                                                                                                               AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGGGGACCTCGGCGCAGCCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-052803/04
DB; AAY52992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
TATGAGATGTGGCGCAACTACCCTTTCTTGTTCGGGGCCCGTGGGCTGCTACTTCAAGACG
                      CTCTTCAGCCTGGCGGTCTCTGACCTCCTGGTCCTTGGAATGCCCCTGGAGGTC
                                                                                                                   TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGTCATTGGCAAT
                                                                                                                                                                    AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
                                                                                                                                                                                                                  ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurotensin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASTRA AB
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                       identify agents for producing anasthesia and analgesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             anasthesia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cao J,
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARMA INC
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                                                                                                                                                                                                                                                                                                                293 A; 423 C; 294 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Donnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                              98.5%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           analgesia
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                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                               Score 717.8; DB Z1;
Pred. No. 1.2e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding cDNA
                                                                                                                                                                                                                                                                                                                350 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ,
                                                                                                                                                                                                                                                                                        DB 21;
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                                                                                                                                                                                                                                                                                       Length 1360;
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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360
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                         24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein coupled receptor; IGS4; IGS4A; IGS4B; schizophrenia; nervous system disorder; psychiatric disorder; Parkinson's disease; episodic paroxysmal anxiety, phobia; migraine; epilepsy; bulimia; stroke; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; cardiovascular disease; heart failure; angina pectoris; obesity; emesis; motility disorder; myocardial infarction; hypertension; dyslipidemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrointestinal disorder; inflammatory bowel disease; osteoporosis; inflammation; infection; pain; cancer; immune disorder: allerav. com
                                                                                                                                                                                                                                                                                                   W0200125269-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF80326
                                                                                      31-JUL-2000;
                                                                                                                                                                                                       25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Splice variant of G-protein coupled receptor IGS4A long version cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF80326 standard;
                                        (SOLV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACC
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                                        SOLVAY PHARM
                                                                                 99NL-1013140.
2000EP-0202683.
2000US-0222047.
                                                                                                                                                                                                       2000WO-EP09584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; pain;
disorder; ss.
                                                                                                                                                         99EP-0203140
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 55..945 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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Best Local Sim
Matches 719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system, psychiatric and central nervous system disorders (e.g. schizophrenia, episodic paroxysmal anxiety, phobia, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a splice variant of the long version of a human G-protein coupled receptor designated IGS4A. IGS4 exists in two polymorphic forms, IGS4 and IGS4B. The IGS4 receptors and IGS4 polynucleotides are useful for preventing, ameliorating or correcting dysfunctions or diseases. These diseases include peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overexpression or altered expression of IGS4.
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                                                                                                                                                                                         24-SEP-1999;
24-SEP-1999;
28-JUL-2000;
31-JUL-2000;
                                                              disorders, or cancers
                                                                      New G-protein coupled receptors and the polynucleotides encoding useful for preventing, ameliorating or correcting nervous system disorders, cardiovascular diseases, dyslipidemias, inflammations,
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/*tag= a /*prize variant of G-protein coupled receptor /product= "splice variant of G-protein coupled receptor IGS4A short version"
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The present sequence encodes a splice variant of the short version human G-protein coupled receptor designated IGS4A. IGS4 exists in polymorphic forms, IGS4A and IGS4B. The IGS4 receptors and IGS4

two

Example 1b; Page 94-95;

102pp;

English.

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hypertension), dyslipidemias, obesity, emesis, gastrointestinal disorders (e.g. inflammatory bowel disease or motility disorders), osteoporosis, inflammations, infections (e.g. bacterial, fungal, protozoan or viral), pain, cancers, immune disorders, allergies, sepsis or gynecological disorders. Agonists or antagonists of IGS4 are effective with regard to disorders of the nervous system, including the central and peripheral nervous systems, disorders of the gastrointestinal system, cardiovascular system, skeletal muscle, thyroid, lung or genitourinary system, or immunological disease. The IGS4 polynucleotides are useful as diagnostic reagents for detecting under-expression, overexpression or altered expression of IGS4.
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Sequence 1594 BP; 370 A; 473 C;
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332 G;
419 T; 0 other;
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Query Match Best Local Similarity

98.5%;

Score 717.8; DB 22; Length 1594; Pred. No. 1.2e-145;

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Search completed: January 17, 2003, 02:34:05 Job time: 272 secs

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729 bp Sequence 1 from Patent EP1090990. AXI39107 AXI39107.1 GI:14274786

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PAT 30-MAY-2001

RESULT 1 AX139107 LOCUS

ALIGNMENTS

REFERENCE AUTHORS TITLE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 729)

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Harland, L.P. Human g-protein-coupled receptor Patent: EP 1090990-A 1 11-APR-2001;

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1 (bases 1 to 801)
Vogelia: Mood, L.S., Parodi, L.A., Hie
Slightom, J., Schellin, K.A., Kaytes, P.S
Sejlitz, T. and Huff, R.M.
Novel g protein-coupled receptors
Patent: WO 0136473 A 17 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Quality: Phrap Quality
Estimated Total Number
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Submitted (03-AUG-1999) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
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Mammalia; Eutheria; Primates; Catarrhini
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DOE Joint Genome Institute and Stanford
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Finishing Completed at Stanford Human Genome
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ive, Walnut Creek, CA 94598, USA
Sep 26, 2001 this sequence version replaced gi:15290296
aft Sequence Produced by DOE Joint Genome Institute
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d Total Number of Errors
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                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1239)
Liu,Q., McDonald,T.P.,
Direct Submission
                                                                                                                                                                                                                                                                                                                             Submitted (09-MAR-2000) Pharmacology, Point, PA 19486, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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                                                                                                                                                           /note="FM-4"
                                                                                                                                                                           /gene="NMU2R"
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McKee, K.K.
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 Homo sapier
Eukaryota;
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AB041228.1 GI:10257380
G protein-coupled receptor
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Chordata; Craniata;
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Pred. No. 2.2e
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JOURNAL
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Best Local S
Matches 719
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Local Similarity 99.7%;
nes 719; Conservative
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Shintani,Y., Moriya,T., Ohkubo,S
Direct Submission
Submitted (03-APR-2000) Yasushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of neuromedin U receptor J. Biol. Chem. 275 (38),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosoya,M., Moriya,T., Kawamata,Y., Ohkubo,S., I
Shintani,Y., Fukusumi,S., Habata,Y., Hinuma,S.,
Nishimura,O. and Fujino,M.
Identification and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
1 (sites)
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Tsukuba, Ibaraki 300-4293, Japan
(E-mail:Shintani_Yasushi@takeda.co.jp, Tel:81-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax:81-298-64-5000)
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/product="G protein-coupled receptor TGR-1"
/protein_id="Babl3721.1"
/protein_id=
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393 c 269 g
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FQNVISSFHKQWHSQHDPQLPPAQRNIFLTECHFVELTEDIGPQFPCQSSMHNSHLPT
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No. 2.
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1.2e-125;
les 2;
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1298)

Raddatz R., Wilson, A. E., Artymyshyn, R., Bonini, J. A., Borowsky, B., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Kouranova, E. V., Nagorny, R., Guevarra, M.S., Boteju, L.W., Zhou, S., Vaysse, P.J., Branchek, T.A., Gerald, C., Forray, C. and Adham, N.

Identification and characterization of two neuromedin U receptors differentially expressed in peripheral tissues and the central
                                                                                                                                                                                                                                                                                          2 (bases 1 to 1298)
Bonini,J.A., Raddatz,R., Wilson,A. and Borowsky,B.
Direct Submission
Submitted (25-MAY-2000) Target Discovery and Assessment,
Pharmaceutical Corporation, 215 College Road, Paramus, N
                                                                                                                                                                                                                                                                                                                                                                                             nervous
J. Biol.
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AF272363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                             Chem.
/product="neuromedin U receptor 2"
/protein_id="AAG24794 1"
/protein_id="AAG24794 1"
/db_xref="G1:10946203"
/translation="MSGMEKLONASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF
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YZEMMRNYPFLEGPVGCYFKTALFETVCFASZLSITTYVSVERYVAILHPERAKLQSTR
RRALRILGIVMGFSVLESLPNTSIHGIKFHYFPNGSLVPGSATCTVIKPMIYNFIIQ
VTSFLFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRCCRKSVNKMLEVLVLV
FAICWAPFHIDRLFFSFYEEWSESLAAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRF
                                                                                                                                                                /gene="NMUR2"
27. .1274
                                                                                                                       /codon_start=1
                                                                                                                                    /note="G
                                                                                                                                                /gene="NMUR2"
                                                                                                                                                                                                    /map="5q31.1-q31.3"
                                                                                                                                                                                                                  /chromosome="5"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                              /organism="Homo
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:10946202
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Mammalia; Eutheria;
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              TTCTACCTCCTCCCCATGACTGTCATCAGTGTCCTCTACTACCTCATGGCACTCAGAGTG
                                                              TGTACGGTCATCAAGCCCATGTGGATCTACAATTTCATCATCCAGGTCACCTCCTTA
                                                                                                                       ATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCGGCCACC
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Deleersnijder, W., Berger, C., Loeken, C.,
Human g-protein coupled receptor
Patent: WO 0135269-A 9 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
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/protein_id="CAC37775.1"
/db_xref="GI:13924116"
/translation="MSGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF
/LPWSVYVPIFVVGVIGNULVCLULQHQAMKTPTNYYLFSLAVSDLLVLLLGMPLE
VYEMWRNYPFLEGSPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTR
RRALRILGIVWGFSVLFSLDNTSIHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQ
VTSFLEYLLPWTVISVLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLSLWRSG
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/db_xref="taxon:9606"
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Patent: WO 0125269-A II 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
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/db_xref="GI:13924118"
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MWRNYPFLFGPVGCYFKTALFETVCFASJLSITTVSVERTVAILHFFRAKLOSTRRA
LRILGIVWGFSVLFSLPNTSLHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTS
FLFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLSLWRSGVNP
WLLCSTSSMWGQVSSST"

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/db_xref="taxon:9606"
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          AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGAGCCAC
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AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCAC
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Patent: WO 0125269-A 1 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                               /protein_id="cac37771.1"
//db_xref="gi:13924108"
//db_xref="gi:13924108"
//db_xref="gi:13924108"
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RRALRILGIVMGFSVLFSLPNTSIHGIKFPFPNGSLVPGSATCTVIKPMMIYNF1IQ
VTSFLFYLLPMTVISVLYXLMALRLKKOKSLEADEGNANIGRECRKSVUKMLFYLVLV
FAICWAPFHIDRLFFSFVEEMSESLAAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRF
OAAFQNVISSFHKOMISQHDDPQLPPAQRNIFLTBCHFVELTEDIGPQFPCQSSMHNSH
DAFGQNVISSFHKOMSHDDPQLPPAQRNIFLTBCHFVELTEDIGPQFPCQSSMHNSH
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                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 to 1658)

Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and v Human g-protein coupled receptor Patent: WO 0125269-A 3 12-APR-2001; Solvay Pharmaceuticals B.V. (NL)

Location/Qualifiers
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                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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VSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLLLGMPLEVYE
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                                                        /codon_start=
                                                                     /note="IGS4A short version"
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FLFYLLDWTVLSVLYVLMALRIKKDKSLEADEGNANIQBPCRSVNKMLFVLVLVFAI
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ALSSEQMSRTNYQSFHENKT"
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             ATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCCCTGGTCCCAGGTTCCGGCCACC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1658)
Deleersnijder,W., Berger,C., Loeken,C., Nys,G. and V
Human 9-protein coupled receptor
Patent: WO 0125269-A 5 12-APR-2001;
Solvay Pharmaceuticals B.V. (NL)
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QAAFQNVISSFHKQWHSGHDPQLPPAQRNIFLTBCHFVELTEDIGPQFLCQSSVHNSH
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FLPVSVYYPFIEVGVLGNULVCLVILOHQAMKTPTNYYLFSLAVSDLLVLLLGMPLE
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RRALRILGIVWGDSVLFSLPNTSIHGIKFHYFFBWGSLVPGSATCTVIKPMWIYMFIQ
QTSFLFYLLDMTVISVLYYLMALRLKKDKSLEADBGNANIQRPCRKSVNKMLFVLVLV
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AX109240.1 GI:13924113
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t: WO 0125269-A 7 12-APR-2001;
y Pharmaceuticals B.V. (NL)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC37774.1"
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fonvissfhkqmhsqhdpqlppagrnifitechfveltbdigpgflcossvhnshlpt
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J. Biol. Chem. 275 (50), 39482-39486 (2000)
                                                                                                                                                                                                                                                                               Pang,L., Wang,S., Laz,T. and Hedrick,J.A. Direct Submission
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/translation="MSGMEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHF FLPVSVVYVPIFVVGVIGNVLVCLVILQHQAMKTPTNYYLFSLAVSDLLVLLCAMPLE VYEMMRNYPFLEGPVGCYFKTALFETVCFAS ILSITTVSVERYVAILHPFRAKLQSTR RRALRILGIVAGFSVLFSLPMTSIHGIKFHYPPMGSLVPGSATCTVIKPMMIYNFIIQ VTSFLFYLLPMTVISVLLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLV
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/chromosome="5"
                                                                      /product="neuromedin U receptor-type
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/db_xref="GI:9944990"
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                                                                                                                 /note="G protein coupled receptor; NmU-R2"
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 Homo
                          MGC
                                    BC016938
BC016938.1
                                                             Homo sapiens,
IMAGE:3852151,
                                                                                       BC016938
sapiens.
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QAAFQNVISSFHKQWHSQHDPQLPPAQRNIFLTECHFVELTEDIGPQFPCQSSMHNSH
LPTALSSEQMSRTNYQSFHFNKT"
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                                                                                                                                                                                                AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGGAGCCTCGGCGCAGCCAC 120
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GTCCTGGTGTGCCTGGTGATTCTGCAGCACCAGGCTATGAAGACGCCCCACCAACTACTAC
                                                                                                                              TTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTTTGTGGTGGGGGGTCATTGGCAAT
                                                                                                                                                                                                                                                                    ATGGAAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAAACTAGAAGATCCATTCCAG
                                                                                     AAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTGCGGACCTCGGCGCAGCCAC
                                                                                                                                                                                                                                                                                                                                                       718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.series: IRAK Plate: 20 Row: n Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA.Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (05-NOV-2001) National Institutes of Health,
Gene Collection (MGC), Cancer Genomics Office, Nationa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: (Di
Dickson, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:
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/product="neuromedin U receptor 2"
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VYEMMRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVERYVALILHPFRAKLQSTR
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LPTALSSEQMSRTNYQSFHFNKT"
1 579 c 411 g 598 t
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VTSFLFYLLPMTVISVLYYLMALRLKKDKSLEADEGNANIQRPCRKSVNKMLFVLVLV
FAICWAPFHIDRLFFSFVEEWSESLAAVFNLVHVVSGVFFYLSSAVNPIIYNLLSRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Colon, adenocarcinoma"
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/lab_host="DH10B"
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/db_xref="Locusin:56923"
/db_xref="taxon:9606"
/clone="MGC:21396 IMAGE:3852151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www<sup>-</sup>shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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99.6%;
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Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hullyk,S., Hume,J., Jackson,L.E., Jackson,L.E., Jackson,E., Kally,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
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Submitted (26-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 165392)
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Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Dep
of Molecular and Human Genetics, Baylor College of Medicine
Baylor Plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version replaced gi:21217312.
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                                                                                                                                                                                                                                                                                                                                                                    is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990339 Consensus quality: 121972 bases at least Q40 Consensus quality: 127005 bases at least Q30 Consensus quality: 130275 bases at least Q20
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Center clone name: CH230-353A10
------ Summary Statistics
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Search completed: January 17, 2003, 04:30:06  $\,$  Job time : 3043  $\,$  secs

OLE: WAY RE JOYE SILL